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APPLICANT: McMichael, Andrew APPLICANT: Hill, Adrian V.S. APPLICANT: Gilbert, Sarah C. APPLICANT: Schneider, Jorg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 7616, A
Sequence 18937, A
Sequence 107, Appl
Sequence 107, Appl
Sequence 20716, A
Sequence 20716, A
Sequence 20716, A
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 22, Appli
Sequence 2, Appli
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                                                                                                                                                                                       December 6, 2004, 15:19:18 ; Search time 27.5 Seconds (without alignments) 21.704 Million cell updates/sec
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-454-204A-41

US-08-313-288B-14

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US-09-228-966-107

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Maximum Match 100%
Listing first 45 summaries
                                                                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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101400000000000000000000000000000000000	ALIGNMENTS 204A Reagents fo ate A CD8 T 9/454,204A	rsion 4.0 rsion 4.0 f the Malar Score 48; D Pred. No. 3. Mismatches
S-09-513-999C-77- S-00-366-623-2 S-08-015-973-8 S-08-081-929-8 S-08-793-410-29 S-08-793-410-29 S-08-793-410-30 S-08-793-410-7 S-09-064-411A-9 S-09-064-411A-9 S-08-464-5238-24 S-08-464-5238-24 S-08-464-6538-24 S-08-464-6538-24 S-08-464-6538-24 S-08-464-6538-3 S-08-460-845D-3 S-08-460-845D-3 S-08-460-845D-3 S-08-460-845D-3 S-08-460-845D-3 S-08-868-458-4	ALIGNMEN 4204A a Reagents rate A CDE 09/454,204 9	Version Version Score Pred. 0; Misr
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128 162 162 162 132 132 133 133 133 141 111 141 111	lication US/09 11 CON: hael, Andrew hael, Adrian V.S. L'Adrian V.S. Arahaman CON: Methods a. CON: Which Ge. 2907.1000-000 CON: Which Ge. 2907.1000-000 DATE: 1999-12 DN NUMBER: DATE: DN NUMBER: PCT	MBER: GB 97 997-06-09 1:78 r Windows V TL Epitope 100.0%; 100.0%; vative 0 9 9
	atic ft, ft, ft, ft, ft, ft, ft, ft, ft, ft,	ATE: 1997 ION WUMBER ATE: 1997 ID NOS: 7 SEQ for W TION: CTL CONSERVAT CONSERVAT NVKYLV 9 NVKYLV 9 NVKYLV 9
	Lical Chilon Control Chilon Ch	TKY] TKY] TKY] TKY] TKY]
	ALI SULT 1 -09-454-204A-20 Sequence 20, Application US/09454204A BAPLEDANT MEMICHAEL, Andrew APPLICANT: MEMICHAEL, Andrew APPLICANT: Gilbert, Sarah C. APPLICANT: Gilbert, Sarah C. APPLICANT: Schneider, Jorg APPLICANT: Plebanski, Magdalena APPLICANT: Smith, Geoffrey L. APPLICANT: MAGDALER, DOWNERS: US/09/45 CURRENT APPLICATION NUMBER: US/09/45 CURRENT FILING DATE: 1999-12-09 PRIOR APPLICATION NUMBER: US/08/08/09 PRIOR APPLICANTON NUMBER: US/08/08/09 PRIOR APPLICANTON NUMBER: US/08/08/09 PRIOR APPLICATION NUMBER: US/08/08/09 PRIOR APPLICANTON NUMBER: US/08/08/08/08/08/08/08/08/08/08/08/08/08/	
	-204A-2 e - 20, A e - 20, A INFORM ANT: B ANT: B	PRIOR FILING D PRIOR FILING D PRIOR FILING D NUMBER OF SEQ SOFTWARE: Fast SOFTWARE: FRT ORGANISM: Unk FEATURE: OTHER INFORM OUTY MATCH Best Local Simi Matches 9; Matches 9; Matches 1 HLG Db 1 HLG Db 1 HLG SEGUIT 2 SEGUIT 2 SEGUIT 2 SEGUIT 2 SEGUIT 2 SEGUIT 3 SEGUIT 4 SEGUIT 5 SEGUIT 6663
	ULT 1 09-454-204 Sequence 20 Sequence 20 Septent No. SENERAL INF APPLICANT: FILE REFER FOR THE THE OF IT TITLE	PRIOR FILLI PRIOR FILLI PRIOR FILLI NUMBER OF SOFTWARE: EQ ID NO 20 LENGTH: 9 TYPE: PRI OFFEATURE: OTHER INFO OFFEATURE: OTHER INFO OFFEATURE: OTHER INFO OFFEATURE: OFFEATURE: OFFEATURE: OFFEATURE: OFFEATURE: OFFEATURE: OFFEATURE: OFFEATURE: OFFEATURE: OFFEATURE: I
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                                                                                                                                                      0; Indels
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Sequence 44, Application US/09009953
Patent No. 6413517
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Identification of Broadly
Reactive DR Restricted Epitopes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER NEADABLE FORM:
COMPUTER READABLE FORM:
COMPUTER I IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE
CONFUMER: PASSESSO for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/009,953
FILING DATE: 21-Jan-1998
CLASSIFICATION : CURROWN>
PRIOR APPLICATION OWNBER: US 60/036,713
FILING DATE: 23-JAN-1997
APPLICATION NUMBER: US 60/037,432
FILING DATE: 07-FEB-1997
ATTORNEY/ABGNT INFORMATION:
ANACOMETER OF TREESTER OF TANACOMETER OF TAN
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REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-011520US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.3%; Score 40; DB 4;
100.0%; Pred. No. 0.092;
                                                                                         100.0%; Score 48; DB 1 100.0%; Pred. No. 0.12;
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
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US-07-846-992-3
Sequence 3, Application US/07846992
; Patent No. 5583046
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TELEFAX: 415-576-0300
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INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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; ANTI-SENSE: NO
US-08-313-288B-14
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US-09-009-953-44
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                                       APPLICANT: Hanke, Truesally APPLICANT: Hanke, Tomas APPLICANT: Hanke, Tomas APPLICANT: Smith, Geoffrey L. APPLICANT: Smith, Geoffrey L. APPLICANT: Blanchard, Tom TTILE OF INVENTION: Which Generate A CD8 T Cell Immune Response; TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response; TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response; TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response; TITLE OF INVENTION NUMBER: US/09/454,204A CURRENT FILING DATE: 1999-12-09 CURRENT FILING DATE: 1998-06-09 PRIOR APPLICATION NUMBER: GB 97 11957.2 PRIOR PILING DATE: 1997-06-09 NUMBER OF SEQ ID NOS: 78 NUMBER OF SEQ ID NOS: 78 SEQ ID NOS: 78 LENGTH: 229
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Sequence 14, Application US/08313288B

Sequence 14, Application US/08313288B

Sequence 14, Application US/08313288B

Setent No: 5750502

GENERAL INFORMATION:
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP STREET: 1103 Avenue of the Americas
CITY: New York
COUNTRY: USA
ZIP: New YORK
COUNTRY: OSSTEM: PC-DOS/MS-DOS
SOFTWARE: PAPELICATION DATA: NO NO NEW YORK
CLASSIFICATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 28,678
TELECOMMUNICATION NUMBER: 28,678
TELECOMMUNICATION NUMBER: 28,678
TELECHONE: (212) 391-0526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 9; Conservative 0; Mismatches 0; Indels
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, OTHER INFORMATION: Complete Epitope of Malaria String US-09-454-204A-41
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                     Plebanski, Magdalena
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 HLGNVKYLV 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 HLGNVKYLV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-08-313-288B-14
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US-09-328-352-7616

; Sequence 7616, Application US/09328352
; Patent No. 6562958
; TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT PILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7616
; LENGTH: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence identity with profilin of other organisms is as follows: 30% with human profilin, 28% with calf and mouse, 26% with yeast and 25% with Acanthamoeba
APPLICANT: Rumpold, Helmut
APPLICANT: Scheiner, Otto
TITLE OF INVENTION: Barch Pollen Allergen Pl4 for Diagnosis
TITLE OF INVENTION: and Therapy of Allergic Diseases
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: New York
COUNTRY: New York
CONTRY: New York
COMPUTER READABLE FORM:
MEDIN TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIN TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIN TYPE: Ploppy disk
COMPUTER: DATE: No. 1925
CURRENT APPLICATION DATA: NO. 1992
APPLICATION NUMBER: US/07/846,992
FLING DATE: 06-JUN-1992
APPLICATION NUMBER: US/07/353,844
FILING DATE: 18-MAY-1992
APPLICATION NUMBER: US/07/353,844
FILING DATE: 18-MAY-1992
APPLICATION NUMBER: 20,280
REPERBURCE/DOCKET NUMBER: 20,280
TELEFRANCE/DOCKET NUMBER: 20,280
TELEFRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h Similarity 66.7%; Pred. No. 1.7; 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Betula verrucosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||| :||:|
68 HLGGIKYMV 76
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 HLGNVKYLV 9
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                             APPLICANT: Valence, Rudolf
APPLICANT: Valence, Michael
APPLICANT: Duchence, Michael
APPLICANT: Brettenbarch, Michael
APPLICANT: Brettenbarch, Michael
APPLICANT: Kraft, Dietrich
APPLICANT: Kraft, Dietrich
APPLICANT: Scheiner, Otto
TITLE OF INVENTION: Birch Pollen Allergen P14 for Diagnosis
TITLE OF INVENTION: and Therapy of Allergic Diseases
CORRESPONDENCE: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.2%; Score 39; DB 1; Length 133; 66.7%; Pred. No. 1.7; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/846,992

FILING DATE: 19920606

CLASSIFICATION: 435

PRIOR APPLICATION 1935

PILING DATE: 18-MAY-1992

ATFORNEY/AGENT INPORMATION:

NAME: Jones III, Harry C

REGISTRATION NUMBER: 20,280

REGISTRATION NUMBER: 6530-011

TELEFRACE/DOCKET NUMBER: 6530-011

TELEFRACE/LOSCET NUMBER: 6130-011

TELEFRACE/LOSCET NUMBER: 100-9990

TELEFRACE/LOSCET NUMBER: 100-9990

TELEFRACE CHARACTERISTICS:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Flappy disk
COMPUTER: IBM PC COMPALING
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08469555; Patent No. 5648242; GENERAL INFORMATION:
APPLICANT: Valenta, Rudolf
APPLICANT: Duchene, Michael
APPLICANT: Pettenburger, Karin; APPLICANT: Breitenburger, Karin; APPLICANT: Kraft, Dietrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Betula verrucosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 133 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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HLGGIKYMV 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-07-846-992-3
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US-08-469-555-3
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Sequence 20116, Application US/09252991A

Sequence 20116, Application US/09252991A

Sequence 20116, Application US/09252991A

GENERAL INFORMATION:
APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PELING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 20716
                                                                                                                                      RESULT 10

US-09-004-393B-4

; Sequence 4, Application US/09004393B
; Patent No. 6310271
; GENERAL INNOFAMATION:
; APPLICANT: Hanson D., Andrew
; APPLICANT: Burnet, Michael
; TITLE OF INVENTION: Polymuclectides Encoding Choline Monooxygenase and
; TITLE OF INVENTION: Plants Transformed Therewith
; FILE REFERENCE: UF-162
; CURRENT APPLICATION NUMBER: US/09/004,393B
; CURRENT FILING DATE: 1998-01-08
; PRIOR FILING DATE: 1998-01-08
; NUMBER OF SEQ ID NOS: 6
; SGO ID NOS: 6
; SEQ ID NO 4

LENGTH: 446
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Gaps
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Indels
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1; Mismatches
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US-09-228-986-107
; Sequence 107, Application US/09228986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-20716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 87.5
Matches 7; Conservative
  7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Beta vulgaris
US-09-004-393B-4
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                                                              140 LGNVEYLV 147
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| 147 LGNVEYLV 154
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    Matches
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LOCATION: (369)

OTHER INDERMATION: Identity of amino acid sequences at the above locations are unknoted us-09-248-796A-18937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: Hanson D., Andrew
APPLICANT: Hanson D., Andrew
APPLICANT: Rathinasabapathi, Bala
APPLICANT: Burnet, Michael
TITLE OF INVENTION: Polynucleotides Encoding Choline Monooxygenase and
TITLE OF INVENTION: Plants Transformed Therewith
FILE REFERENCE: US-162
CURRENT APPLICATION NUMBER: US/09/004,393B
CURRENT FILING DATE: 1998-01-08
PRIOR PELICATION NUMBER: 60/035,147
PRIOR FILING DATE: 1997-01-08
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO. 2.0
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Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 75.0%; Score 36; DB 4; Length 376; Best Local Similarity 75.0%; Pred. No. 23; Matches 6; Conservative 2; Mismatches 0; Indels
                                                                                 Score 37; DB 4; Length 265; Pred. No. 9.7;
                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09004393B Patent No. 6310271
    ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.0%;
87.5%;
                                                                                 77.1%;
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; ORGANISM: Spinacia oleracea
US-09-004-393B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Candida albicans
                                                                                   Query Match 77.1
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 HLGSLKYL 133
                                                                                                                                                                                                       81 HLGEVSYLV 89
                                                                                                                                                                   1 HLGNVKYLV 9
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Best Local Similarity
                                                                                                                                                                                                                                                                                       US-09-248-796A-18937
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Pred. No. 46;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Chang, Yuan
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Unique Associated Kaposi's Sarcoma
TITLE OF INVENTION: Virus Sequences And Uses Thereof
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS: ADDRESSE: Cooper & Dunham
STREET: 1185 Avenue of the Americas
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION WUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45185-B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                          SOFTWARE: PATCHILI Release #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/420,235B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,101A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-343-101A-22
; Sequence 22, Application US/08343101A
; Patent No. 5830759
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                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 4:
TELECOMMUNICATION INFORMATION
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 70.8%;
Best Local Similarity 75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 301 amino acids TYPE: amino acid
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                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 HLGSVSYL 182
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                                                                                                                                                     ZIP: 10036
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Sequence 107, Application US/10101464A

Patent No. 678041

GENERAL INFORMATION:

APPLICANT: Strabala, Timothy

APPLICANT: Nieuwenhuizen, Nicolaas

FILE OF INVENTION: Compositions Isolated from Plant Cells

FILE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling

FILE OF INVENTION: 2002-03-18

FILE OF INVENTION NUMBER: 09/704,302

PRIOR FILING DATE: 2000-11-01

PRIOR FILING DATE: 1999-01-12

PRIOR FILING DATE: 1999-11-01

PRIOR FILING DATE: 1999-11-01

PRIOR FILING DATE: 2000-01-11

PRIOR FILING DATE: 2000-01-11
                     APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID MOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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PAREENL No. 5801042
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Moore, Partick S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 70.8%; Score 34; DB 3; Length 150; Best Local Similarity 62.5%; Pred. No. 21; Matches 5; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.8%; Score 34; DB 4; Length 150; 62.5%; Pred. No. 21; indels tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 107
TENGTH: 150
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 62.5'
"--rhes 5; Conservative
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US-10-101-464A-107
                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Pinus radiata
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101 HLGNISFL 108
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US-08-420-235B-47
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LENGTH: 150
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Search completed: December 6, 2004, 15:32:09 Job time: 28.5 secs

Sequence 118, App Sequence 118, App Sequence 191, App Sequence 158, Ap Sequence 158, Ap Sequence 19, Appl Sequence 11929, A Sequence 65501, A Sequence 65501, A Sequence 65501, A Sequence 6510, A Sequence 6510, A Sequence 6510, A Sequence 6510, A Sequence 191246, Sequence 6510, A Sequence 6510, A Sequence 6510, A

Sequence 165, App Sequence 108, App Sequence 108, App

Sequence 1, Appli

Sequence Sequence

Sequence 63190, A Sequence 55223, A Sequence 58005, A Sequence 58005, A Sequence 69639, A

Sequence 41, Appl Sequence 41, Appl Sequence 41, Appl Sequence 164906, Sequence 44, Appl Sequence 44, Appl

Sequence

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Sequence 1, Application US/10042202
Publication No. US20020136733A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
Catherine Elizabeth Margaret ALLSOPP, Ajit LALVANI, Magdalena PLEBANSKI, Hilton Carter WHITTLE,
TITLE OF INVENTION: MALARIA PEPTIDES
NUMBER OF SEQUENCES: S.2
CORRESPONDENCE ADDRESS:
ADDRESSEE: WENDEROYH, LIND & PONACK, L.L.P.
STREET: 2033 K Street, N.W., Suite 800,
CITY: Washington
COMPTRY: U.S.A.
ZIP: 2006-1021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
. SOFTWARE: WordPad for Windows 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/042,202
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6, Appli
89, Appl
11, Appl
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                                                                                                                                   December 6, 2004, 15:26:21 ; Search time 99 Seconds (without alignments) 32.420 Million cell updates/sec
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-673-674-20
US-10-673-624-20
US-10-873-473-508
US-10-873-745-20
US-10-877-745-20
US-10-877-217-508
US-10-686-943-20
US-10-686-943-20
US-10-10-167-89
US-10-74-167-89
US-10-775-167-89
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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Database :

Result Š.

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Run on:

Searched:

Gilbert, Sarah C.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 48; DB 13; Length 9; 100.0%; Pred. No. 1.4e+06;
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Sequence 20, Application US/10079167
Sequence 20, Application US/10079167
Sequence 20, Application US/10079167
SERNERAL INFORMATION:
APPLICANT: Hill, Adrian V.S.
APPLICANT: McShane, Helen
APPLICANT: Reece, William
APPLICANT: Schneider, Joerg
ITILE OF INVENTION: Vaccination Method
FILE REPERBNCE: 2907.1000-001
CURRENT FILING DATE: 2007-02-19
FRIOR APPLICATION NUMBER: US/90/91/67
CURRENT FILING DATE: 1999-12-09
FRIOR FILING DATE: 1998-06-09
FRIOR FILING DATE: 1998-06-09
FRIOR FILING DATE: 1998-06-09
FRIOR FILING DATE: 1997-06-09
FRIOR FILING DATE: 1997-06-09
FRIOR FILING DATE: 2001-09-13
FRIOR FILING DATE: 2001-09-13
FRIOR FILING DATE: 2001-09-13
FRIOR FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 99
LINNGRANE: SEC ID NOS: 99
LINNGTH: 90
LINNGRH: 90
LINNGTH: 90
LIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-042-202-1
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Sequence 20, Application US/10653624
Publication No. US20040131594A1
GENERAL INFORMATION:
APPLICANT: McMichael, Andrew
APPLICANT: Hill, Adrian V.S.
TELECOMMUNICATION INFORMATION:
TELEFAN: (202)-721-8250
TELEFAN: (202)-721-8250
TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                      LENGTH: 9 amino acids
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.0
Matches 9, Conservative
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US-10-079-167-20
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US-10-777-055-508

Sequence 508, Application US/1077053

publication No. US20040132088A1

general Sos, Application US/1077053

publication No. US20040132088A1

APPLICANT: Diamond, David C.

APPLICANT: Diamond, David C.

APPLICANT: Diamond, David C.

APPLICANT: Out, Zhiyong

APPLICANT: Lei, Xiang-Dong

TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF

TITLE OF INVENTION: EXPRESSION VECTORS AND METHODS FOR THEIR DESIGN

TITLE OF INVENTION: 2004-02-10

PRIOR PEPLICATION NUMBER: 10/292,413

PRIOR PILING DATE: 2004-11-07

PRIOR FILING DATE: 2001-11-07

NUMBER OF SEQ ID NOS: 979

SEQ ID NO 508

LENGTH: 9
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APPLICANT: Schneider, John APPLICANT: Schneider, John Schneider, John Schneider, John Schneider, John Schneider, John Spellcant: Hanke, Tomas APPLICANT: Hanke, Tomas APPLICANT: Blanchard, Tomas APPLICANT: Blanchard, Tom TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response FILE REFERENCE: 2907.1000-000

FILE REFERENCE: 2907.1000-000

FILE REFERENCE: 2907.1000-000

FILE REPERENCE: 1999-12-09 002

PRIOR APPLICATION NUMBER: US/09/454,204A

PRIOR APPLICATION NUMBER: ECT/GB98/01681

PRIOR FILING DATE: 1998-06-09

PRIOR FILING DATE: 1998-06-09

PRIOR FILING DATE: 1997-06-09

NUMBER OF SEQ ID NOS: 78

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTHER DATE: DATE

LENGTHER DATE

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Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: CTL Epitope of the Malaria String
US-10-653-624-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 48; DB 16;
100.0%; Pred. No. 1.4e+06;
tive 0; Mismatches 0;
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; ORGANISM: Plasmodium Faciparum
US-10-777-053-508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-10-833-439-20
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Sequence: 508, Application US/10837217
Publication No. US20040203051A1
GENERAL INFORMATION:
APPLICANT: Simard, John J. L.
APPLICANT: Diamond, David C.
APPLICANT: Lei, Xiang-Dong
TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
FILE REPERBNCE: MANNK. 02222
CURRENT APPLICATION NUMBER: US/10/837,217
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                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hanke, Tomas
APPLICANT: Hanke, Tomas
APPLICANT: Smith, Geoffrey L.
APPLICANT: Blanchard, Tom
TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response
FILE REFERENCE: 2907.1000-000
CURRENT APPLICATION NUMBER: US/10/686,943
PRIOR APPLICATION NUMBER: US/10/686,943
PRIOR APPLICATION NUMBER: US/09/454,204
PRIOR PLILNG DATE: 2003-10-16
PRIOR PLILNG DATE: 2003-10-16
PRIOR PLILNG DATE: 1999-12-09
PRIOR FILING DATE: 1999-06-09
PRIOR FILING DATE: 1998-06-09
PRIOR FILING DATE: 1998-06-09
PRIOR FILING DATE: 1998-06-09
PRIOR FILING DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PESTSEQ for Windows Version 4.0
SEQ ID NO 20
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; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: CTL Epitope of the Malaria String
US-10-833-745-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: CTL Epitope of the Malaria String US-10-833-744-20
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ilarity 100.0%; Pred. No. 1.4e+06;
Conservative 0; Mismatches 0;
                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20, Application US/10833744
Publication No. US20040197349A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: McMichael, Andrew
APPLICANT: Hill, Adrian V.S.
APPLICANT: Gilbert, Sarah C.
APPLICANT: Schneider, Jorg
APPLICANT: Plebanski, Magdalena
                                                                                                                                                                                                                                                                                                                                                                       1 HLGNVKYLV 9
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Best Local Similarity
Matches 9; Conserv
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ORGANISM: Unknown
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Publication No. US20040191272A1

GENERAL INPORMATION:

APPLICANT: Mill, Adrian V.S.

APPLICANT: Gilbert, Sarah C.

APPLICANT: Schneider, Jords

APPLICANT: Schneider, Jords

APPLICANT: Schneider, Jords

APPLICANT: Blanchard, Tomas

APPLICANT: Blanchard, Towas

APPLICANT
                                                                                                                                                                                                                                              APPLICANT: Hanke, Tomas
APPLICANT: Hanke, Tomas
APPLICANT: Hanke, Tomas
APPLICANT: Smith, Geoffrey L.
APPLICANT: Blanchard, Tom
APPLICANT: Blanchard, Tom
TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response
FILE REFRERENCE: 2907.1000-000
CURRENT APPLICATION NUMBER: US/10/686,943
PRIOR APPLICATION NUMBER: US/10/686,943
PRIOR APPLICATION NUMBER: US/09/454,204
PRIOR PILING DATE: 2003-10-16
PRIOR PILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1998-06-09
PRIOR FILING DATE: 1998-06-09
PRIOR FILING DATE: 1998-06-09
SPRIOR PRIOR PRIOR NUMBER: GB 97 11957.2
PRIOR PRIOR DATE: 1998-06-09
SOOFWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
; OTHER INFORMATION: CTL Epitope of the Malaria String
US-10-833-439-20
Sequence 20, Application US/10833439
Publication No. US20040175365A1
GENERAL INFORMATION:
                                                                                                                               Hill, Adrian V.S.
Gilbert, Sarah C.
Schneider, Jorg
Plebanski, Magdalena
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ORGANISM: Unknown
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US-10-833-745-20
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APPLICANT: Hill, Adrian V.S.
APPLICANT: Gilbert, Sarah C.
APPLICANT: Gilbert, Sarah C.
APPLICANT: Gilbert, Sarah C.
APPLICANT: Schneider, Jorg
APPLICANT: Hanke, Tomas
APPLICANT: Hanke, Tomas
APPLICANT: Banchard, Tom
APPLICANT: Blanchard, Tom
APPLICANT: Blanchard, Tom
TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response
FILE REPERBNCE: 2907.1000-000.
TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response
FILE REPERBNCE: 2907.1000-000.
CURRENT APPLICATION NUMBER: US/10/466,943
CURRENT FILING DATE: 1999-1-0.0
PRIOR PILING DATE: 1999-1-0.0
PRIOR FILING DATE: 1999-1-0.0
PRIOR FILING DATE: 1999-0.0
PRIOR FILING DATE: 1997-0.0
PRIOR PRIOR FILING DATE: 1997-0.0
PRIOR OF TOWARE: PRESENCE FARENCE OF WINDOWS VERSION 4.0
SOFTWARE: PRESECT FOR WINDOWS VERSION 4.0
SEQ ID NO 20
LENGTH: 9
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Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: CTL Epitope of the Malaria String US-10-686-943-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
CURRENT FILING DATE: 2004-04-30
PRIOR APPLICATION NUMBER: 10/292,413
PRIOR FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: 60/336,968
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 979
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 508
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20, Application US/10686943
Publication No. US20040213799A1
GENERAL INFORMATION:
APPLICANT: McMichael, Andrew
                                                                                                                                                                                                                                                           ; ORGANISM: Plasmodium Faciparum
US-10-837-217-508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
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US-10-360-836-6
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TITLE OF INVENTION: PARTICLES TO DEVELOP VACCINES AGAINST INFECTIOUS PATHOGENS TITLE OF INVENTION: AND MALIGNANCIES FILE REFERENCE: 5986/1J876 CURRENT APPLICATION NUMBER: US/10/360,836 CURRENT FILING DATE: 2003-02-07 PRIOR APPLICATION NUMBER: 60/354,963 PRIOR FILING DATE: 2002-02-08 NUMBER OF SEQ ID NOS: 86 SOFTWARE: FASTES OF TOWN OF SEQ ID NOS: 86 SOFTWARE: PASTES OF TOWN OF TW
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US-10-079-167-89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 48; DB 14; Length 15; Best Local Similarity 100.0%; Pred. No. 0.019; Matches 9; Conservative 0; Mismatches 0; Indels
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Sequence 89, Application US/10079167

Publication No. US20030138454A1

GENERAL INFORMATION:

APPLICANT: Hill, Adrian V.S.

APPLICANT: GIALBER, Sarah C.

APPLICANT: Reece, William

APPLICANT: Schneider, Joerg

TILE REPERBNCE: 2907.1000-001

CURRENT APPLICATION NUMBER: US/10/079,167

CURRENT APPLICATION NUMBER: US/10/079,167

CURRENT FILING DATE: 1999-12-09

PRIOR PILING DATE: 1999-12-09

PRIOR PILING DATE: 1998-06-09

PRIOR FILING DATE: 1998-06-09

PRIOR FILING DATE: 1997-06-09

PRIOR FILING DATE: 1997-06-09

PRIOR FILING DATE: 1997-06-09

PRIOR PILING DATE: 1997-06-09

PRIOR PILING DATE: 1997-06-09

PRIOR PILING DATE: 2001-09-13

PRIOR PILING DATE: 2001-09-13

PRIOR PILING DATE: 2001-09-13

PRIOR PILING DATE: 2001-09-21

NUMBER OF SEQ ID NOS: 99

LENGTH: 20
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; Publication No. US2004001817A1
GENERAL INFORMATION:
APPLICANT: OXXON PHARMACCINES LIMITED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Plasmodium
US-10-360-836-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Unknown
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US-10-345-000-11
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GENERAL INCORMATION

GENERAL INCORMATION

GENERAL INCORMATION

APPLICANT: Hill, Adrian V.S.

APPLICANT: Hill, Adrian V.S.

APPLICANT: Schneider, Jozah C.

APPLICANT: Schneider, Jozah C.

APPLICANT: Schneider, Jozah C.

APPLICANT: Plebanski, Magdalena

APPLICANT: Blanchard, Tomas

APPLICANT: Blanchard, Tomas

APPLICANT: Blanchard, Tomas

APPLICANT: Blanchard, Tomas

APPLICANT: Mich Geoffrey L.

APPLICANT: Mich Geoffrey L.

APPLICANT: Mich Generate A CD8 T Cell Immune Response

FILE REFERENCE: 2907.1000.000

CURRENT PILING DATE: 2004-04-28

PRIOR APPLICATION NUMBER: US/10/488,943

PRIOR APPLICATION NUMBER: US/09/454,204

PRIOR APPLICATION NUMBER: BCT/GB98/01681

PRIOR PILING DATE: 1998-06-09

PRIOR FILING DATE: 1997-06-09

SEQ ID NO 41

LENGTH: LESTERE C.

LENGTH
                                            APPLICANT: Hanke, Tomas
APPLICANT: Smith, Geoffrey L.
APPLICANT: Blanchard, Tom
TITLE OF INVENTION: Methods and Reagents for Vaccination
TITLE OF INVENTION: Methods and Reagent For Vaccination
FILE REFERENCE: 2907.1000-000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 48; DB 16; Length 229;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 48; DB 16; Length 229; 100.0%; Pred. No. 0.33; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Complete Epitope of Malaria String US-10-653-624-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
; OTHER INFORMATION: Complete Epitope of Malaria String
US-10-833-439-41
                                                                                                                                                                                                                                         CURRENT PEDLICATION NUMBER: US/10/653,624
CURRENT FILING DATE: 2003-09-02
PRIOR APPLICATION NUMBER: US/09/454,204A
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1998-06-09
SPRIOR FILING DATE: 1998-06-09
SOFTWARE: PRESEQ FOR WINDOWS VERSION 4.0
SOFTWARE: PRESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 41
LENGTH: 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 41, Application US/10833439
Publication No. US20040175365A1
GENERAL INFORMATION:
           Plebanski, Magdalena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Unknown
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ORGANISM: Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 48; DB 15; Length 20; Best Local Similarity 100.0%; Pred. No. 0.026; Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hill, Adrian V.S.
APPLICANT: Hill, Adrian V.S.
APPLICANT: McShane, Helen
APPLICANT: Garbert, Sarah C.
APPLICANT: Rece, William
APPLICANT: Schneider, Joerg
TITLE OF INVENTION: Vaccination Method
FILE REPRENCE: 2907.1000-001
CURRENT APPLICATION NUMBER: US/10/079,167
CURRENT PILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: US 09/454,204
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: GB 97 11957.2
PRIOR APPLICATION NUMBER: GB 97 11957.2
PRIOR APPLICATION NUMBER: GB 97 11957.2
PRIOR PILING DATE: 1997-06-09
PRIOR PILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: GB 00 23203.3
PRIOR APPLICATION NUMBER: GB 023203.3
PRIOR FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 99
TITLE OF INVENTION: VACCINATION METHOD FILE REFERENCE: 550-409 CURRENT APPLICATION NUMBER: US/10/345,000 CURRENT FILING DATE: 2003-02-20 NUMBER OF SEQ ID NOS: 21 SOFTWARE: Patentin version 3.0 SEQ ID NO 11 LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 41, Application US/10079167
Publication No. US20030138454A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: McMichael, Andrew APPLICANT: Hill, Adrian V.S. APPLICANT: Gilbert, Sarah C. APPLICANT: Schneider, Jorg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 HLGNVKYLV 11
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LENGTH: 229
TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                US-10-345-000-11
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US-10-653-624-41
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Gaps

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Mon Dec 6 15:42:47 2004

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Search completed: December 6, 2004, 15:36:07 Job time : 100 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

6, 2004, 15:18:43; Search time 23.5 Seconds (without alignments) 36.849 Million cell updates/sec December

US-10-042-202-1 48 1 HLGNVKYLV 9 Title: Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir1:*
pir2:*
pir3:* PIR 79:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

KIES	Description	thrombospondin-re	sporozoite surface	profilin - Europea	I ga	myosin I myr 4 -	et.	hypothetical prote	profilin - Para ru	hypothetical prote	choline monooxygen	choline monooxygen	hypothetical prote	conserved hypothet	myosin heavy chain	hypothetical prote		v			_	•	hypothetical prote	hypothetical prote	ATP-dependent RNA	alpha-1 proteinase	myosin-RhoGAP prot	guanine-nucleotide	phosphopantetheine	
SUMMERTES	QI	S04531	A46283	JC2082	C45438	A53933	S63345	T25693	T10769	T22736	T09214	T14542	T27936	D83196	T18296	D39999	T21412	T24349	A26655	S33042	T15219	H81319	E97776	H71702	\$13653	A29953	T31099	297	B95230	0
	DB	~	~	8	~	~	~	7	~	~	7	~	~	7	~	~	~	7	~	~	~	7	7	~	~	~	N	~	~	•
	Query Match Length	559	574	133	427	1006	384	450	131	317	439	446	495	536	2139	347	408	1017	2116	301	348	461	260	560	604	785	2626	123	162	000
	Query Match	100.0	100.0	81.2	81.2	81.2	77.1	77.1	75.0	75.0	75.0	75.0	75.0	75.0	75.0	72.9	72.9	72.9	72.9	70.8	70.8	70.8	70.8	70.8	70.8	70.8	70.8	œ.	68.8	0
	Score	48	48	39	39			37	36					36	36				35	34	34	34	34	34	34	34		33		
	Result No.	-	7	e	4	S	9	7	80	O	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	90

•	hypothetical prote	dipeptide ABC tran	carbonate dehydrat	hypothetical prote	propionate kinase	oleoyl-[acyl-carri	oleoyl-[acyl-carri	hypothetical prote	probable ABC trans	conserved hypothet	myosin-VIIa motor	probable ATP-depen	hypothetical prote	hypothetical prote	myosin VIIa, short	probable unconvent	
	A83906	D64557	CRHU6	T24947	AH0896	A59034	T12583	B96534	B84825	A81682	A59285	S62003	C89940	T32487	A59257	E84726	
	7	~	-	N	N	~	N	~	~	N	N	N	N	N	~	0	
	222	285	308	311	402	412	430	494	544	266	999	617	733	843	1203	1490	
	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	
	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	
	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

```
Thrombospondin-related protein TRAP - malaria parasite (Plasmodium falciparum)
N;Alternate names: thrombospondin-related anonymous protein
C;Species: Plasmodium falciparum
C;Species: O7-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S04531
R;Robson, K.J.H.; Hall, J.R.S.; Jennings, M.W.; Harris, T.J.R.; Marsh, K.; Newbold, C.I., Nature 335, 79-82, 1988
A;Title: A highly conserved amino-acid sequence in thrombospondin, properdin and in prote A;Reference number: S04531
A;Reference number: S04531, MUID:88318952; PMID:3045563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: DNA
A,Residues: 1-559 <ROS
A;Cross-references: UNIPROT:P16893; EMBL:X13022; NID:g9977; PID:g9978
F;240-287/Domain: thrombospondin type 1 repeat homology <FHR1>
RESULT
                                                    804531
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100.0%; Score 48; DB 2; Length 559; 100.0%; Pred. No. 0.15;

Gaps ö 0; Indels 0; Mismatches Query Match 100. Best Local Similarity 100. Matches 9; Conservative

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3 HLGNVKYLV 11 0 1 HLGNVKYLV 원 ઠે

Sporozoite surface protein 2 - malaria parasite (Plasmodium falciparum) (strain NF54)
N'Alternate names: thrombospondin-related anonymous protein (TRAP)
C'Species: Plasmodium falciparum
C'Species: D6-Jan-1995 #text_change 09-Jul-2004
C'Accession: A46283
R'Rogers, W.O.; Malik, A.; Mellouk, S.; Nakamura, K.; Rogers, M.D.; Szarfman, A.; Gordon, Proc. Natl. Acad. Sci. U.S.A. 89, 9176-9180, 1992
A'Reference number: A46283; MUD:93028427; PMID:1409621
A'Accession: A46283
A'Status: preliminary; nucleic acid sequence not shown; translation not shown
A'Residues: 1-574 «ROGS»
A'Residues: 1-574 «ROGS»

A;Cross-references: UNIPROT:Q26020; GB:M94013; NID:g160690; PID:g160691 F;240-287/Domain: thrombospondin type 1 repeat homology <THR1>

Gaps ö Similarity 100.0%; Score 48; DB 2; Length 574; Similarity 100.0%; Pred. No. 0.15; 9; Conservative 0; Mismatches 0; Indels Local Similarity Query Match Best Local S: Matches 9

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Gaps

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Acticuse type: DNA
A;Residues: 1.450 kMIL-
A;Kesidues: 1.450 kMIL-
A;Cross-references: UNIPROT:002150; EMBL:U97549; PIDN:AAB52849.1; GSPDB:GN00028; CESP:F1!
A;Experimental source: strain Bristol N2; clone F15A8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein YNR015w - yeast (Saccharomyces cerevisiae)
NiAlternate names: hypothetical protein N2065
CiSpecies: Saccharomyces cerevisiae
CiSpecies: Saccharomyces cerevisiae
CiDate: 27-Apr.1996 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
CiAccession: S63343; S63343, S63346
R;Duesterhoeft, A.; Floch, M.; Fritz, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, aubmitted to the Protein Sequence Database, April 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                        Score 39; DB 2; Length 1006;
Pred. No. 17;
3; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yeast (Saccharomyces cerevisiae)
protein N2065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Readidues: 1-554 cDDR>
A; Cross-references: UNIPROT: P53720; EMBL: Z71630; MIPS:YNR015w
A; Experimental source: strain S288C
R; Maurer, C.T.C.; Urbanus, J.H.M.; Planta, R.J.
submitted to the Protein Sequence Database, April 1996
A; Reference number: S63266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-58 «MAU»
A;Cross-references: EMBL:Z71630; MIPS:YNR015w
A;Experimental source: strain S288C
A;Expell, T.M.
submitted to the Protein Sequence Database, April 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rimiller, N. submitted to the EMBL Data Library, April 1997 A;Description: The sequence of C. elegans cosmid F15A8 A;Reference number: 220069
F_112-682/{\rm Domain}: {\rm myosin} {\rm motor} {\rm domain} {\rm homology} {\rm < MMOT>} F_1102-109/{\rm Region}: {\rm nucleotide-binding motif} {\rm A} ({\rm P-loop})
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: SGD:SNM1
A;Cross-references: SGD:S0005298; MIPS:YNR015w
A;Map position: 14R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Reference number: S63346
A.Accession: S63346
A.Molecule type: DNA
A.Residues: 336-384 < POH>
A.Experimental source: strain S288C
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                                                                                                                Query Match 81.2%;
Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 55...
For Si Conservative
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289 HIGNTKYML 297
                                                                                                                                                                                                                                                                                                                    |||||:|::|
276 HLGNLKFIV 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: S62944
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-Mar-2004
C;Accession: C45438
R;Sherr, E.H.; Joyce, M.P.; Greene, L.A.
J. Cell Biol. 120, 1405-1416, 1993
A;Title: Mammalian myosin I alpha, I beta, and I gamma: new widely expressed genes of th A;Reference number: A45438; MUID:93194946; PMID:8449986
A;Accession: C45438
                                                                                                                profilin - European white birch
NyAlternate names: actin-binding protein
Cispecies: Betula pendula (European white birch)
Cispecies: Betula pendula (European white birch)
Cispecies: 14-01-1994 #sequence_revision 14-011-1994 #text_change 09-Jul-2004
Cispecies: 14-01-1994 #sequence_revision 14-011-1994 #text_change 09-Jul-2004
Cispecies: 15-010-1994 #sequence_revision 01-1994 #text_change 09-Jul-2004
Cispecies: No.; Ball, T., Vortal 18, Juchene, M.; Kraft, D.; Scheiner, O.
Biochem. Biophys. Res. Commun. 199, 106-118, 1994
A;Title: CDNA cloning and expression of timothy grass (Phleum pratense) pollen profilin
A;Reference number: JC2080; MUID: 94168560; PMID: 8123000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: JC2082
A;Molecule type: mRNA
A;Roseuces: 1-133 <VAL>
A;Croseuces: UNIPROT:P25816
A;Experimental source: pollen
C;Comment: This protein is responsible for cross-reactivities in 20% of pollen and food
C;Superfamily: profilin
C;Keywords: actin binding; cytoskeleton
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A53933

myosin I myr 4 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Accession: 1994 #sequence_revision 07-Oct-1994 #text_change 02-Feb-2001

C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 02-Feb-2001

C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 02-Feb-2001

C;Accession: A53933

R;Baehler, M; Kroschewski, R.; Stoeffler, H.E.; Behrmann, T.

J. Cell Biol. 126, 375-389, 1994

J. Cell Biol. 126, 375-389, 1994

A;Title: Rat myr 4 defines a novel subclass of myosin I: identification, distribution, A;Reference number: A53933

A;Accession: A53933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.2%; Score 39; DB 2; Length 427; 66.7%; Pred. No. 6.8; 0; Indels ive 3; Mismatches 0; Indels
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66.7%; Pred. No. 2;
Live 2; Mismatches
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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132 HLGNLKFIV 140
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HLGGIKYMV 76
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                                                            RESULT 3
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R'Rathinasabapathi, B.; Burnet, M.; Russell, B.L.; Gage, D.A.; Liao, P.C.; Nye, G.J.; Scr
Proc. Natl. Acad. Sci. U.S.A. 94, 3454, 1997
A;Title: Choline monooxygenase, an unusual iron-sulfur enzyme catalyzing the first step c
A;Reference number: Z16612; MUID:97250559; PMID:9096415
                                                                                                                                                                                                                                                                                                                                                                        A;Accession: T09214
A;Status: translated from GB/EMBL/DDBJ
A;Nolecule type: mRNA
A;Rolecule type: mRNA
A;Rosidues: 1-439 <RAT>
A;Rosidues: 1-439 <RAT>
A;Cross-references: UNIPROT:O04121; EMBL:U85780; NID:g1943944; PIDN:AAB52509.1; PID:g194:
A;Note: parts of this sequence, including the amino end of the mature protein, were deten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Keywords: 2Fe-2S; chloroplast; metalloprotein; oxidoreductase; Rieske iron-sulfur prote F;1-60/Domain: transit peptide (chloroplast) #status predicted <TRP>F;61-60/Domain: transit peptide (chloroplast) #status predicted <TRP>F;61-439/Product: choline monooxygenase #status experimental <MAT>F;152-199/Domain: Rieske [2Fe-2S] homology <RRS. F;152-199/Domain: Rieske [2Fe-2S] cluster (Cys, His, Cys, His) (covalent) #status p)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-446 <RUS>
A;Cross-references: UNIPROT:O22553; EMBL:AF023132; NID:g2522209; PID:g2522210
A;Experimental source: strain Great Western D-2; salinized leaves
A;Note: expression induced by osmotic stress
                 holine monooxygenase (BC 1.1.3.-) precursor - spinach
;Species: Spinacia oleracea (spinach)
;Bate: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004;Accession: T09214
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.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
.Accession: T14542
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27936
R;Leimbach, D.
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75.0%; Score 36; DB 2; Length 439;
Best Local Similarity 87.5%; Pred. No. 28;
Matches 7; Conservative 1; Mismatches 0; Indels
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A;Description: The sequence of C. elegans cosmid ZK622.
A;Reference number: Z20443
A;Accession: T27936
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A;Molecule type: DNA
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Pred. No. 28;
1; Mismatches
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Best Local Similarity 87.5%;
Matches 7; Conservative 1
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147 LGNVEYLV 154
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A;Cross-references: UNIPROT:Q9XUY5; EMBL:Z81550; PIDN:CAB04477.1; GSPDB:GN00028; CESP:F5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribeturias, J.A.; Arilla, M.C.; Gomez-Bayon, N.; Martinez, J.; Martinez, A.; Palacios, submitted to the EMBL Data Library, October 1997
A, Description: Cloning and expression of profilin allergen from Hevea brasiliensis.
A, Reference number: 217130
A, Steession: T10769
A, Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cofilin - Para rubber tree
;Species: Hevea brasiliensis (Para rubber tree)
;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
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Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                   Score 37; DB 2; Length 450;
Pred. No. 18;
3; Mismatches 0; Indels
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                                       A;Gene: CESP:F15A8.7
A;Map position: X
A;Introns: 30/3; 80/3; 140/2; 172/1; 250/3; 285/3; 375/3
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C;Superfamily: Na+/K+-transporting ATPase beta chain
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submitted to the EMBL Data Library, November 1996
A;Reference number: 219607
A;Accession: T22736
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: mRNA
A,Residues: 1-131 <AST>
A,Cross-references: UNIPROT:065812; EMBL:Y15042
A,Experimental source: cv. RRIC 133; pollen
C,Superfamily: profilin
C,Keywords: actin binding; cytoskeleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Superfamily: profilin
;Keywords: actin binding; cytoskeleton
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Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 66.
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240 HIGDVEYLV 248
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66 HLGGTKYMV 74
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235 HLGKVKYI 242
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C;Genetics:
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A; Residues: 1-495 < LEI>

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6, 2004, 15:31:09
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 16-Aug-2004
C;Accession: D93196
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bx adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: D83196
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A/Rodecule type: DNA
A;Rosiques: 1-2139 <GUI>
A;Cross-references: UNIPROT:Q07569; EMBL:L03534; NID:g1850912; PID:g1850913; PIDN:AAB480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q9HX24; GB:AE004780; GB:AE004091; NID:g9949749; PIDN:AAG0699
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein PA3602 [imported] - Pseudomonas aeruginosa (strain PAO1)
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A,Cross-references: UNIPROT:Q23552; EMBL:U39998; PIDN:AAA81102.1; CESP:ZK622.3 C;Genetics: A;Genetics: CESP:ZK622.3 A;Genetics: CESP:ZK622.3 A;Introns: 34/2; 97/2; 222/3; 310/3 C;Superfamily: Caenorhabditis elegans hypothetical protein ZK622.3
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C;Species: Entamoeba histolytica
C;Species: Cot-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18296
R;Guillen, N.
Submitted to the EMBL Data Library, February 1997
A;Reference number: Z18865
A;Accession: T18296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h Similarity 75.0%; Score 36; DB 2; Length 536; Similarity 75.0%; Pred. No. 34; 6; Conservative 2; Mismatches 0; Indels
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C;Superfamily: myosin heavy chain; myosin motor domain homology
F;91-780/Domain: myosin motor domain homology <MMO>
                                                                                                                                                                  75.0%; Score 36; DB 2; Length 495; 66.7%; Pred. No. 32; tive 1; Mismatches 2; Indels
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A;Gene: PA3602
C;Superfamily: Glutamate synthase, large subunit domain 2
                                                                                                                                                                     Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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64 LGNIRYLV 71
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Matches 6; Conserv
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A;Residues: 1-536 <STO>
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Silusher, M.B.; Gregory, J.; Storey, C.C.; Richmond, S.J.

Submitted to the EMBL Data Library, October 1991

A; Description: Analysis of the complete nucleotide sequence of the plasmid pCpAl isolated
A; Reference number: $18141

A; Recession: $18145

A; Status: preliminary

A; Molecule type: DNA

A; Molecule type: DNA

A; Molecule type: DNA

A; Residues: 1-347 < LUS>

A; Residues: 1-347 < LUS>

A; Cross-references: UNIPROT: Q46260; EMBL: X62475; NID: 940608; PIDN: CAA44336.1; PID: 940613
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ypothetical protein 4 - Chlamydophila psittaci
;Species: Chlamydophila psittaci, Chlamydia psittaci
;Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 09-Jul-2004
;Accession: S18145; D39999
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DT 17AP
CO TRAP
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Q70g43 plasmodium
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O7176 plasmodium
O7176 plasmodium
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                                                                    December 6, 2004, 15:17:52 ; Search time 125.5 Seconds (without alignments) 41.262 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 2000000000
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09tyd1
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NCBI_TaxID=5833;
                                                                                                                                                                                                                                                    Name-trap;
Plasmodium falciparum.
Bukaryota, Alveolata; Apicomplexa, Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                             Mamillapalli A., Joshi H., Malhotra P.;
Mamillapalli A., Joshi H., Malhotra P.;
Submitted (Aug-2003) to the EMBL/GenBank/DDBJ databases.
SMBL; AJS81768; CAR46495-1; -.
InterPro; IPR000884; TSP1.
InterPro; IPR00091; VWFA.
Pfam; PF00092; VWA-1.
Pfam; PF00092; VWA-1.
Pfam; PF00453; VWFADOMAIN.
SWART; SM00209; TSP1; 1.
SWART; SM00209; TSP1; 1.
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Last annotation update)
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
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100.0%; Pred. No. 0.4
tive 0; Mismatches
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SEQUENCE FROM N.A.
STRAIN=BM3-62;
Mamillapalli A., Joshi H., Malhotra P.;
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PROSITE; PS50234; VWFA; 1.
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 Trap protein (Fragment)
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PRINTS; PR00453; VWFADOMAIN
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Mamillapalli A., Joshi H., Malhotra P.;
Mamillapalli A., Joshi H.crminal region of Plasmodium falciparum in
Indian isolates.";
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
"Polymorphism in TRAP-N terminal region of Plasmodium falciparum in
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Nameetrap;
Plasmodium falciparum.
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5833;
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Mamillapalli A., Joshi H., Malhotra P.;
Submitted (ANG-2046) to the EMBL/GenBank/DDBJ databases.
BMBL; AJS8171; CAE4648.1; -.
InterPro; IPR000884; TSP1.
InterPro; IPR002035; WFA.
Pfam; PF00092; TSP 1.
                                         Indian isolates.";
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ581768; CAE4495.1; -.
NON_TER 323 323
                                                                                                                                                                                                                    323 AA; 36608 MW; 02A0030CC5EDCA93 CRC64;
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CAE46498;
02-MAR-2004 (TEMBLrel. 27, Last sequence update)
02-MAR-2004 (TEMBLrel. 27, Last sequence update)
02-MAR-2004 (TEMBLrel. 27, Last annotation update)
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SMART; SM00209; TSP1; 1.
SMART; SM00207; VWB; 1.
PROSITE; PS50092; TSP1; 1.
PROSITE; PS50234; VWFA; 1.
NON TER 327 327
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es 9; Conservative C
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Q70GJ7
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CAE46498
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                               Length 327;
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Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ581770; CAE46497.1; -.
InterPro; IPR002084; TSP1.
InterPro; IPR002035; VWF.A.
Pfam; PF00090; TSP J; 1.
Pfam; PF00092; VWA, 1.
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ582081; CAE46626.1; -.
InterPro; IPR002084; TSP1.
InterPro; IPR002035; VWF.A.
Pfam; PF00092; TSP.].
Pfam; PF00092; VWA, 1.
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EMBL, AJ581771; CAE46498.1; -.
NON TER 327 327
SEQÜENCE 327 AA; 37251 MW; 881D7A4B4EDD235A CRC64;
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Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                             . Match 100.0%; Score 48; DB 2; Local Similarity 100.0%; Pred. No. 0.44; les 9; Conservative 0; Mismatches 0.
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05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
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SMART; SM00209; TSP1; 1.
SMART; SM00327; VWA; 1.
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Best Local Similarity 100.00
Best ag 9; Conservative
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3 HLGNVKYLV 11
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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plasmodium falciparum.
Eukaryodia, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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EMBL, AJS81769; CAE44646-1; -.
EMBL, AJS81769; CAE44646-1; -.
InterPro; IPR000884; TSP1.
InterPro; IPR000884; TSP1.
Ffam; PR00090; TSP 1; 1.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00329; VWFADOMAIN.
SMART; SM00329; VWFADOMAIN.
PROSITE; PS500327; VWFADOMAIN.
PROSITE; PS500327; VWFADOMAIN.
PROSITE; PS50034; VWFA; 1.
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Mamillapalli A., Joshi H., Malhotra P.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJSSH1767, CAE46494.1; -.
InterPro; IPR00884; TSP1.
InterPro; IPR002035; VWF_A.
SMART; SM00209; TSP1; 1.
SMART; SM00327; VWA; 1.
PROSITE; PS50092; TSP1; 1.
NON TER 331 331
SEQÜENCE 331 AA; 37521 MW; CBD1823A0C8C49EB CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Q70GJ9;
05-JUL-2004 (
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SEQUENCE
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Q70GK1;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=trap;
Jasmodium falciparum.
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                 DB 2; Length 331;
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100.0%; Pred. No. 0.44;
tive 0; Mismatches 0; Indels
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Mamillapalli A., Joshi H., Malhotra P.;

Mamillapalli A., Joshi H., Malhotra P.;

Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AJ581765; CAE46493.1; -.

InterPro; IPR000884; TSP1.

InterPro; IPR002035; VWF A.

Pfam; PF00092; VWA, 1.
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Mamillapalli A., Joshi H., Malhotra P.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
Pfam; PF00030; TSP_1; 1.
Pfam; PF00032; VWA; 1.
PRINTS; PR00433; VWFADOWAIN.
SMART; SM00327; VWA; 1.
PROSITE; PS50034; VWFA; 1.
PROSITE; PS50234; VWFA; 1.
NON_TER 331 331 331
SEQÜENCE 331 AA; 37601 MW; 39EBBACF0DD9C77C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           331 AA; 37609 MW; 2FE4EB47F1963D76 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Trap protein (Fragment).
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                    100.0%; Score 48; DB 2; 100.0%; Pred. No. 0.44;
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SMART; SM00209; TSP1; 1.
SMART; SM00327; VWA; 1.
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 9; Conservative
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Mamillapalli A., Joshi H., Malhotra P.;
Mamillapalli A., Joshi H., Malhotra P.;
Mamillapalli A., Joshi H., Malhotra P.;
Mondran isolates.",
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AJS81769, CAE46496.1;
SUDMITER 331
SEQÜENCE 331 AA; 37573 MW; 60EBBAC3FDD9C779 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=BK3-17;
Mamillapalli A., Joshi H., Malhotra P.;
Mamillapalli A., Joshi H., Malhotra P.;
Molina isolates.";
Submitted (Ang-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ581767; CAE46494.1;
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Eukaryota, Alveolata, Apicomplexa; Haemosporida; Plasmodium.
1101_TaxID=5833;
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Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 9; Conservative 0; Mismatches 0; Indels
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                         Length 331;
                                                                                                                                       0; Indels
                        331 331 330 MW; 2FB4EB47F1963D76 CRC64;
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SEQÜENCE 331 AA; 37601 MW; 39EBBACF0DD9C77C CRC64;
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
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CAE46496;
CAE46496;
02-MAR-2004 (TEMBLrel. 27, Last sequence update)
02-MAR-2004 (TEMBLrel. 27, Last sequence update)
                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 9; Conservative 0; Mismatches 0
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EMBL, AJ581765; CAE46493.1; -. NON TER 331 331 SEQÜENCE 331 AA; 37609 MW;
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TRAP.
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ID CAE4
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Mamiliapalli A., Joshi H., Malhotra P.;
Mamiliapalli A., Joshi H., Malhotra P.;
Maniliapalli A., Joshi H., Malhotra P.;
Indian isolates..;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=RM3-51;
Mamillapalli A., Joshi H., Malhotra P.;
Mamillapalli A., Joshi H., Malhotra P.;
Monitoral isolates.";
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AJS81764; CAR46492.1; -..
SEQÜENCE 331 AA; 37625 MW; 4258443729D48835 CRC64;
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NCBL_TaxID=5833;
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NCBL_TaxID=5833;
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                                                                                                                                                                                                                                                                                                         100.0%; Score 48; DB 2; Length 331; 100.0%; Pred. No. 0.44; tive 0; Mismatches 0; Indels
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CAE46493,
CAEA-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
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02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Trap protein (Fragment).
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       EMBL; AJ581764; CAE46492.1; -.
InterPro; IPR000884; TSP1.
InterPro; IPR000155; VWP.A.
Pfam; PF00009; TSP 1; 1.
Pfam; PF00092; VWA; 1.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00209; TSP1; 1.
PROSITE; PS0092; TSP1; 1.
PROSITE; PS0092; TSP1; 1.
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Best Local Similarity 100.
Matches 9; Conservative
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RESULT 15

CAE46497

ID CAE46497

DT CAE46497

DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DT TRAP Drotein (Fragment).

CA TRAP (TRAP A)

CA ENGARYOLA: Alveolata; Apicomplexa; Haemosporida; Plasmodium.

CA NCBI TAXID=5833;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=CM3-56;

RA Mamillapali A., Joshi H., Malhotra P.;

RT 'Polymorphism in TRAP-N terminal region of Plasmodium falciparum in RT Indian isolates."

RT 'Polymorphism in TRAP-N terminal region of Plasmodium falciparum in RT Indian isolates."

RT 'RD SEQUENCE AJ3 A33 A33 A3521 MW; CBD1823AOC8C49EB CRC64;

COURTY MATCH 331 A3, 37521 MW; CBD1823AOC8C49EB CRC64;

COURTY MATCH 100.0%; Pred. NO. 0. 0.44;

Best Local Similarity 100.0%; Pred. NO. 0. 44;

Best Local Similarity 100.0%; Pred. NO. 0. 44;

Best Local Similarity 0, Mismatches 0; Indels 0; Gaps 0;
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Search completed: December 6, 2004, 15:30:15 Job time : 126.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

December 6, 2004, 15:14:37 ; Search time 119 Seconds (without alignments) 27.131 Million cell updates/sec Run on:

US-10-042-202-1 48 1 HLGNVKYLV 9

Title: Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2002273 segs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

geneseqq1980s:*
geneseqp21980s:*
geneseqp2001s:*
geneseqp2001s:*
geneseqp2003s:*
geneseqp2003ss:*
geneseqp2003bs:* A_Geneseq_23Sep04:* 1: geneseqp1980s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de			SOFFERES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
П	48	100.0	0	7	AAR87267	Aar87267 Plasmodiu
2	48	100.0	σ	~	AAY10523	Aay10523 HLA Class
٣	48	100.0	6	~	AAY03670	Aay03670 Amino aci
4	48	100.0	6	'n	ABG80206	
2	48	100.0	6	æ	ADK69145	Adk69145 Epitope l
9	48	100.0	6	00	ADQ10943	Adq10943 Plasmodiu
7	48	100.0	15	7	ADE79950	Ade79950 Plasmodiu
8	48	100.0	20	'n	AA017442	Aao17442 P falcipa
6	48	100.0	229	7	AAY03681	Aay03681 Amino aci
10	48	100.0	559	N	AAR05427	
11	40	83.3	15	7	AAW85142	Aaw85142 Helper T-
12	39	81.2	123	4	ABM00029	Abm00029 Allergen
13	39	81.2	133	~	AAR22261	Aar22261 P14 aller
14	39	81.2	133	~	AAR71926	Aar71926 Birch pol
15	39	81.2	133	~	AAY25650	Aay25650 Betula sp
16	39	81.2	133	φ	AAE31498	Aae31498 Birch tre
17	39	81.2	133	7	ADC34899	Adc34899 Tree alle
18	38	79.2	753	4	AAM79139	Aam79139 Human pro
19	38	79.2	764	4	AAM80123	Aam80123 Human pro
20	38	79.2	1006	9	ABP98831	Abp98831 Human str
21	38	79.2	1006	7	ADJ95090	Adj95090 Novel NOV
22	37	77.1	131	ø	AAE31507	7
23	37	77.1	157	4	AAG72436	Aag72436 Human OR-
24	37	77.1	157	4	AAG72246	Aag72246 Human olf
25	37	77.1	265	ø	ADA36329	Ada36329 Acinetoba

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100.0%; Score 48; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels

1	Human olf	3 Pear Pyr	Latex Hev	Latex Hev	5 Latex Hev	3 Latex Hev	5 O.europae	5 O. europae	_	_	Olive tre	~	_	1 Oil-assoc	3 C album c	C album c	ບ່	C. Album	
Adh30958	Aag71620	Aae31518	Aae3150	Aae3150	Aae3150	Aae3150	Aaw7844!	Aaw7844	Aaw7844	Aae3151	Aae3151	Aae3151	Abm00025	Adj 49584	Aag6263	Aag6263	Abg7094	Abg70942	
ADH30958	AAG71620	AAE31518	AAE31504	AAE31509	AAE31506	AAE31508	AAW78445	AAW78446	AAW78440	AAE31512	AAE31511	AAE31513	ABM00025	ADJ49584	AAG62633	AAG62635	ABG70944	ABG70942	
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ALIGNMENTS

RESU AAR8	RESULT 1 AAR87267 Th. AAR87367 standard, montide, 9 aa
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AS S	AAR87267;
i E	16-MAY-1996 (first entry)
X l	
OB A	Plasmodium falciparum HLA-A2 epitope tr26.
\$ 3	Thrombosnondin-related anonomis profess, human lengosote antigen, HLA.
KA	
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SO	Plasmodium falciparum.
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Z,	NOVOLOVIAL
\$ B	12-0CT-1995.
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PF	31-MAR-1995; 95WO-GB000737.
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A ;	(ISIS-) ISIS INNOVATION LID.
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1 t	HILL AVS. AIGOO M, ALLBODD CEM, LGIVAIL A, FIEDGHEKI M;
4 \$	William DO
\$ 2	WDT. 1005_150504/45
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ę fa	Dlasmodium falcinarum nentide(s) - useful in vaccine compositions for
Td	adainst malaria.
X	
	Claim 1; Page 18; 23pp; English.
X ,	
ຽ	Two Gambian individuals showed CTL responses to HLA-A2 peptides tr26,
ខ	tr29 and tr39 (AAR87267-R87269) derived from Plasmodium falciparum
ပ္ပ	thrombospondin-related anonymous protein (TRAP). All three of these
ပ္ပ	peptides bound to HLA-A2 in an assembly assay. Peptide tr39 was
ပ္ပ	-A2-restricted epitope.
ខ្ល	and variants of them) are useful in vaccines against malaria
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Ö	peducine y wy;

AAY03670 standard; peptide; 9 AA.

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AAY03670
                                The present invention describes a method of inducing and/or sustaining an immunological cytotoxic T lymphocyte (CTL) response in a mammal: The method comprises: (a) delivering an antigen to the mammal at a level to induce an immunological CTL response in the mammal; and (b) maintaining the level of the antigen in the mammal's lymphatic system to maintaining the lemunologic CTL response. The method can be used for the delivery of e.g. adifferentiation antigen, a tumour-specific multilineage antigen, an embryonic antigen, an oncogene antigen, a mutated tumour-suppressor gene antigen, or a viral antigen. They can be used for the treatment of disease such as cancer, e.g. malignant melanoma or infectious disease, e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery to the lymphatic system provides for potent CTL stimulation that takes blace in the milleu of the lymphoid organ, and it sustains stimulation that takes blace in the milleu of the lymphoid organ, and it sustains stimulation that takes blace in the milleu of the lymphoid organ, and it sustains stimulation that takes bear of the lymphatic system the milleu of the lymphatic system the lymphatic system the milleu of the lymphatic system the milleu of the lymphatic system the system the system the lymphatic system the system the system the system that system the system that system the system
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inducing a cytotoxic T lymphocyte response - by maintaining a level of antigen in the lymphatic system of a mammal so as to provide a sustained CTL response, used to treat, e.g. AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system; immunisation; tumour; infectious disease; immunotherapy; cancer; malignant melanoma; viral disease; hepatitis; AIDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    HLA Class I motif peptide SEQ ID NO:453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 44; 199pp; English.
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                                                                                                                                                                                                                                                    AAY10523 standard; peptide; 9 AA
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97US-00988320.
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Best Local Similarity 100.9
                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
Plasmodium falciparum.
                                      σ
                                                                                         HLGNVKYLV 9
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10-DEC-1997;
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IID AAY1

AAX

AAX

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AAXI

BDE HLA

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MO99

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The invention relates to mechods and reagents to generating a procedure of the invention relates to mechods at least one target antigen. The kits of the invention comprises (i) as priming composition, a source of one or antigen, plus a carrier I lymphocytes-(CTL) epitopes of the target cardidate and (ii) as boosting composition a source of CTL epitopes, with at least one CTL epitope the same as used in (1), with this source being a non-replicating or replication-impaired recombinant the source being a non-replicating or replication-impaired recombinant to poxvixus vector (PVV) plus a carrier. If the source of CTL epitopes in (1) is a viral vector, then the vector in (ii) is from a different virus. The kits are used to generate an immune response (prophylactic or therapeutic) against pathogens or tumours, specifically against malaria parasites pathogens. The Kits are also used for protective viral or parasitic pathogens. The Kits are also used for protective viral or parasitic pathogens. The Kits are also used for protective viral or parasitic pathogens. The Kits are also used for protective viral or beneficial provide an excellent booster effect, better than that the specified PVV provide an excellent booster effect, better than that protection against sporturing in complete rather than partial protection against sports callenge. Also PVV are safer to use than wild-type virus. Sequences AAV03661-680 represent CTL peptide epitopes of the malaria (M) string
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                   CD8+ T-cell; immune response; antigen; priming composition; CTL; epitope; cytocoxic T lymphocyte; boosting; poxvirus vector; PVV; pathogen; tumour; malaria; parasite; P. falciparum; viral; bacterial; parasitic; cancer; melanoma; HIV; breast; colon; vaccination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to methods and reagents for generating a protective
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Generating CD8-positive T cell response to target antigen using recombinant poxvirus - for treating or preventing malaria and HIV infection, also epitope strings from Plasmodium and HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVS, Gilbert SC, Schneider J, Plebanski M;
Blanchard T;
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                                                                                                                                              Amino acid sequence of the malaria (M) string CTL epitope Tr26.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-GB001681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97GB-00011957.
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                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum.
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Hanke T, Smith GL,
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Best Local Similarity
Matches 9; Conserv
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                                                                             07-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-DEC-1998.
AAY03670;
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RESULT 4 ABG80206

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HLGNVKYLV

RESULT 3

epitope liberation; substrate; proteasome; cytostatic; antibacterial; protecozoaide; fungicide; T-cell activator; vaccine; housekeeping epitope; cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell; virus; bacterium; protozoan; fungus; housekeeping proteasome system.

Epitope liberation-related peptide SeqID508

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The invention relates to a method of inducing and/or sustaining an immunological cytotoxic T lymphocyte (CTL) response in a mammal comprising administering directly to the lymphatic system of the mammal:

(a) an antigen in the form of a polypeptide; (b) a vector comprising a nucleic acid encoding the antigen; or (c) a non-peptide antigen. The certor inducing and/or sustaining CTL response in a mammal. This is particularly useful for treating a mammal having a malignant tumour (e.g. carcinoma, melanoma, leukaemia or lymphoma) or infectious disease (e.g. hepatitis, acquired immune deficiency syndrome (AIDS), malaria, measles or tuberculosis), or in an animal having a predisposition to these diseases. The mammal may be dogs, cats, mice, cattle, sheep, pigs, goate, rabbits, or in an animal having a step. ABG80319 represent viral epitopes on major histocompatibility complex (WMC) class I molecules, used in the method of the invention. (Updated on 29-AUG-2003 to standardise OS field)
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                                                                                                                                                                  Major histocompatibility complex; MHC; MHC class I molecule; virus; epitope; cytotoxic T lymphocyte response; CTL response; lymphatic system; entigen; immunogenic; malignant tumour; carcinoma; malanoma; leukaemia; lymphoma; infectious disease; hepatitis; malaria; measles; tuberculosis; acquired immune deficiency syndrome; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inducing or sustaining immunological cytotoxic T lymphocyte response in a mammal, useful for treating a mammal with malignant tumor or infectious disease, by directly administering an antigen to the lymphatic system of
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                                                                                                                                    WHC class I molecule, viral epitope #454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 37; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CTLI-) CTL IMMUNOTHERAPIES CORP.
ABG80206 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                         22-JAN-2002; 2002WO-US002033
                                                                                                                                                                                                                                                                                                                                                                                                                                               02-FEB-2001; 2001US-00776232
                                                                                                (first entry)
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                                                                              (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-657506/70.
                                                                                                                                                                                                                                                                                                                               WO200262368-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9 AA;
                                                                          29-AUG-2003
15-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                     15-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kundig TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the mammal
                                        ABG80206;
                                                                                                                                                                                                                                                                                          Viruses.
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Identifying polypeptide suitable for epitope e.g., housekeeping epitope, liberation by contacting substrate polypeptide comprising epitope of interest, with proteasome, and assaying for liberation of epitope.

Lei X;

Qiu Z,

Diamond DC,

Simard JJL,

WPI; 2004-167209/16.

07-NOV-2002; 2002US-00292413. 07-NOV-2001; 2001US-0336968P.

(SIMA/) SIMARD J J L. DIAMOND D C.

(DIAM/) DIAMOND (QIUZ/) QIU Z. (LEIX/) LEI X.

Plasmodium falciparum

US2003228634-A1

11-DEC-2003.

Disclosure; SEQ ID NO 508; 67pp; English

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Sultable for epitope of interaction, including the steps of latentrying an epitope of interact; providing substrate pormple steps or latentrying and the epitope, wherein the substrate permits processing by a proteasome; contacting the substrate with a composition including the proteasome; under conditions that support processing of the substrate by proteasome; and assaying for liberation of epitope. The invention may be useful for the development of compounds with a cytostatic, antibacterial, protozoacide or fungicide activity acting as T-cell activators. In addition, the invention may allow development of a vaccine. The invention, where the epitope is a housekeeping epitope. The compositions comprising the identified housekeeping epitope. The compositions comprising the identified housekeeping epitope. The compositions comprising the identified housekeeping epitopes are useful in vitro in vaccine (CTL) to be used in adoptive immunotherapy. The invention is also useful for activating T-cells against neoplastic cells, and cells infected with virus, bacterium, protozoan or fungus. CTL epitopes are identified based on the knowledge that such epitopes are, in fact, produced by the housekeeping proteasome system. Once identified, these epitopes, embodied as a peptides, can be used to successfully immunise or induce therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTL responses against housekeeping proteasome expressing target cells in the host. The present sequence is that of a peptide which is related to the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to a novel method of identifying a polypeptide suitable for epitope liberation, including the steps of identifying a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 48; DB 8; L
100.0%; Pred. No. 1.7e+06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADQ10943 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9 AA;
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Matches
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ADQ10943
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ADK69145 standard; peptide; 9 AA.

RESULT 5 ADK69145 (first entry)

06-MAY-2004

ADK69145;

BXXXXXX

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antimalarial; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                               WO2003066833-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200224224-A2
                                                                                                                                                                                                                                                                               core particle.
                                                      Plasmodium sp
                                                                                                     14-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA017442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
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AAO17442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                       frame comprising a first sequence, where the first sequence encodes one or more segments of tumour-associated antigen SSx-2, which comprises a caquence of 188 amino acids (SEQ ID NO: 40), where the first sequence does not encode the compilers SSX-2 antigen, and where each segment comprises an epitope cluster, the cluster comprising or encoding at least two amino acid sequences having a known or predicted affinity for a same MHC receptor peptide binding cleft. Also described are: an isolated polypeptide comprising the amino acid sequence encoded in the reading frame, and an immunogenic composition comprising (1) or the polypeptide of (1). (1) is a mucleic acid encoding a tumour-associated antigen SSX-2 composition acids (SEQ ID NO: 40). The nucleic acid, the encoded antigen, and composition are useful in including an immune response and in treating cancer. Expression cassettes are used in vaccine vectors. This is the amino acid sequence of a T-cell compositions which is the manno acid sequence of a T-cell compositions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium epitope #6 for method to augment CD8+ T-cell immune response.
                                         immunostimulant; cytostatic; vaccine; tumour-associated antigen SSX-2; SSX-2 antigen; epitope cluster; MHC receptor peptide binding cleft; immunosenic composition; immuno response; cancer; vaccine vector; epitope liberation; human leukocyte antigen; HLA A2-specific CTL; cytotoxic T lymphocyte; T-cell epitope.
                                                                                                                                                                                                                                                                                                                                                     nucleic acid encoding tumor-associated antigen SSX-2, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 48; DB 8; Length 9; 100.0%; Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                inducing an immune response and in treating cancer
                     Plasmodium falciparum T-cell epitope segid 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 508; 260pp; English.
                                                                                                                                                                                                                                                                                                        Lei X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADE79950 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                         Qiu Z,
                                                                                                                                                                                     10-FEB-2004; 2004US-00777053.
                                                                                                                                                                                                           07-NOV-2001; 2001US-0336968P.
07-NOV-2002; 2002US-00292413.
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Best Local Similarity luv...
Best Local Similarity luv...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    described in the invention
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23-SEP-2004 (first entry)
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D
                                                                                                                                                                                                                                             SIMARD J J L.
DIAMOND D C.
QIU Z.
LEI X.
                                                                                                                 Plasmodium falciparum.
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                                                                                                                                                                                                                                                                                                        Diamond
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                                                                                                                                        US2004132088-A1.
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                                                                                                                                                               08-JUL-2004.
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ID ADE7
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AC ADE7
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DT 29-1
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DE Plat
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Tuberculosis, TB, vaccination, vaccine, CD4+ T cell immune response, poxvirus vector; HTV; malaria; Helicobacter pylori; influenza; hepatitis; viral infection; leprosy; protozoan parasite; cancer; tuberculostatic; anti-HIV; protozoacide; antibacterial; virucide; hepatotropic; antileframmatory; antileprotic; cytostatic; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method of generating an immune response against a non-hepadnaviral antigen in a mammal by administering (to the mammal) at least 1 dose of a priming component comprising a recombinant hepatitis B core particle (rHEP) (which is a carrier for 1 or more non-hepadnaviral CD8+ T-cell epitopes of the antigen). The method may be supplemented by the use of a boosting stage comprising a non-replicating or replication-impaired recombinant poxvirus vector. The method is useful for generating an immune response against a non-hepadnaviral antigen in a mammal for treating or preventing cancer or malaria. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Generating an immune response against a non-hepadnaviral antigen in a mammal, useful for treating or preventing cancer or malaria, by administering a priming component comprising a recombinant hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                            non-hepadnaviral antigen; hepatitis B core particle; CD8+ T-cell; epitope; poxvirus vector; cancer; malaria; epitope.
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; Pred. No. 0.013;
0; Mismatches 0; Indels
vaccine; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P falciparum TRAP CD4+ T cell epitope #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 57; SEQ ID NO 6; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYNY-) UNIV NEW YORK MEDICAL CENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                     07-FEB-2003; 2003WO-US003897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-FEB-2002; 2002US-0354963P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zavala F, Birkett AJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD8+ T-cell; immune response; antigen; priming composition; CTL; epitope; cytocoxic T lymphocyte; boosting; poxvirus vector; PVV; pathogen; tumour; malaria; parasite; P. falciparum; viral; bacterial; parasitic; cancer; melanoma; HIV; breast; colon; vaccination.
                                                                                                                                                                  Inducing CD4+ T-cell response against target antigen by administering a composition comprising a source of CD4+ epitopes which is a non-replicating or replication impaired recombinant poxvirus vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 48; DB 5; Length 20; 100.0%; Pred. No. 0.019; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of the malaria (M) string CTL epitope.
                                                                                                     Schneider J;
                                                                                                    Reece W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gilbert SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY03681 standard; protein; 229 AA.
                                                                                                    Gilbert S,
                                                                                                                                                                                                                                        Example 2; Page 32; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mcmichael AJ, Hill AVS, Gilbert
Hanke T, Smith GL, Blanchard T;
                                                                  (OXXO-) OXXON PHARMACCINES LTD
                                 21-SEP-2000; 2000GB-00023203.
13-SEP-2001; 2001WO-GB004116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-GB001681
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                                                                                                  Hill AVS, Mcshane H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum.
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                                                                                                                                    WPI; 2002-394098/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-070325/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY03681;
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The invention relates to methods and reagents for generating a protective CD8+ T-cell immune response against at least one target antigen. The kits of the invention comprises (i) as priming composition, a source of one or more CD8+ T-cell [cytotoxic T lymphocytes-(CTL)] epitopes of the target antigen, plus a carrier and (ii) as boosting composition a source of CTL epitopes, with at least one CTL epitope the same as used in (i), with this source being a non-replicating or replication-impaired recombinant poxvirus vector (PVV) plus a carrier. If the source of CTL epitopes in (i) is a viral vector, then the vector in (ii) is from a different virus. The kits are used to generate an immune response (prophylactic or therapeutic) against pathogens or tumours, specifically against malaria parasites such as P. falciparum, or HIV, and also many other bacterial,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                        viral or parasitic pathogens. The kits are also used for protective responses against melanoma and cancer of breast or colon, and generally wherever a strong CDB+ response is protective. The boosting composition may be used alone to boost a naturally primed response against malaria. The specified PVV provide an excellent booster effect, better than that from wild-type poxvirus, resulting in complete rather than partial protection against sporozoite challenge. Also PVV are safer to use than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA cloned from Plasmodium falciparum - used to prepare polypeptide(s) used in vaccines for persons suffering from or at risk from malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
             Generating CD8-positive T cell response to target antigen using recombinant poxvirus - for treating or preventing malaria and HIV infection, also epitope strings from Plasmodium and HIV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum; malaria; vaccine; ss.
               Generating CD8-positive T cell response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Circumsporozoite (CS)-related protein.
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                                                                                         Example 1; Page 20; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum; T.9/96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised) (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 HLGNVKYLV 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 HLGNVKYLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ02047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-AUG-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-OCT-2003
25-MAR-2003
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Matches
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Matches
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                                                      parasite. The CS related protein can be used to produce vaccines. The antibodies can be used for purificn. of the polypeptides. The vector may be a recombinant virus, esp. baculovirus or the peptide can be chemically prepared. Fragments of the peptide preferably contain a conserved sequence, egresidues 244 to 291 and more particularly a polypeptide selected from the following group: AN WDEWSPCSVTCGGGRESKR B) WDEWSPCSVTCGGGRES (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to grand 24-007-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T-cell peptide; human leucocyte antigen; HLA; DR4w4; DR1; DR7;
                                                                                                                                                                                                                                                                                    Gaps
                                             CS protein is produced during the merozoite stage of the malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Composition containing peptide that induces cytotoxic T lymphocyte response, and helper peptide - can bind to human leucocyte antigen alleles, used to treat or prevent cancers, parasitic infections and autoimmune disease.
                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytotoxic T lymphocyte; CTL; hepatitis; autoimmune disease; acquired immune deficiency syndrowe; malaria; cancer; allograft rejection, allorgy; Lyme disease; hepatitis; post-streptococcal endocarditis; glomerulonephritis;
                                                                                                                                                                                                                                                      100.0%; Score 48; DB 2; Length 559; 100.0%; Pred. No. 0.8;
                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helper T-cell peptide derived from a TRAP protein.
                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      AAW85142 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 37; Slpp; English.
                 Disclosure; Page ?; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0036713P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-US001373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                     9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                             HLGNVKYLV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EPIM-) EPIMMUNE INC.
                                                                                                                                                                                                                                                                                                                 σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-427679/36
                                                                                                                                                                                                                                                                                                                 1 HLGNVKYLV
                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                            Sequence 559 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9832456-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JAN-1997;
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                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW85142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helper
                                                                                                                                                                                                field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  food
                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
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AAW85138-283 represent helper T-cell peptides, which can bind to the human leucocyte antigens (HLA) DR4w4, DR1 and DR7. The peptides are used in the course of the invention. The specification describes peptides that that induce a cytocoxic T lymphocyte (CTL) response, and T-helper peptides, that are used together to generate a CTL response for the

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The invention relates to selecting a protein variant having modified immunogenicity, compared to a parent protein, comprising using the antibody binding sequence to localise epitope sequences on the three dimensional structure of the parent protein and defining an epitope area including amino acids within 5 Angstrom of the epitope amino acids. The method is useful for identifying structural epitopes on the 3-dimensional surface of commercial and environmental allergens. Compositions are containing the protein variants are used as vaccines, detergents and personal care compositions, e.g. shampoo, balsam, hair conditioners, hair waving compositions, hair dyeling compositions, hair tonic, hair liquid, hair cream, hair rinse, hair spray, chewing gum, skin cream, sunscreen, shaving foam, cream soap, skin milk or foundation. The present sequence is that of a polypeptide of the invention
                                                                                                                                                                                                                           ö
treatment or prevention of viral, fungal, bacterial or parasitic infections (e.g. hepatitis, acquired immune deficiency syndrome or malaria) or cancer (e.g. renal or cervical carcinoma, lymphoma, prostate cancer or condyloma acuminatum). Helper T-cell peptides may be used alone to induce a helper T cell response, e.g. in cases of autoimmune disease, allograft rejection, allergy, Lyme disease, hepatitis, post-streptococcal endocarditis, glomerulonephritis and food hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Allergen; protein coordinate data; vaccine; antiallergic; immunogenicity; detergent; personal care composition; cosmetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Selecting protein variants having modified immunogenicity, used to produce vaccines, detergents and personal care compositions, involves localizing epitope sequences on the three-dimensional structure of a
                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                         Length 15;
                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                         DB 2;
0.54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Allergen profilin-birchpollen SEQ ID NO 20.
                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                           Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 67; Page 495; 513pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               ABM00029 standard; protein; 123 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Svendsen A,
                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                           83.3%; 8
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2001DK-00000327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2001; 2001US-0277817P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-APR-2001; 2001WO-DK000293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-APR-2000; 2000DK-00000707.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                               8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roggen EL, Ernst S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NOVO ) NOVOZYMES AS
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                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                         1 LGNVKYLV
                                                                                                                                                                                                                                                                    LGNVKYLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 123 AA;
                                                                                                                                                        Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200183559-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LO-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-APR-2003
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The birch pollen allergen protein P14 (AAR71926) is encoded by the CDNA sequence AAQ89191. The allergen has affinity for poly(L-proline); the use of poly(L-proline) for affinity purification or for in vitro diagnosis of P14 and highly similar proteins is claimed. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                            Use of poly(L-proline) in in vitro diagnosis of P14 birch allergen. - as substitute for antibody, also for allergen purification and recovery from
                                                                                                                                                                            114. .133
/label= epitope
/note= "when coupled to beta-galactosidase, this peptide
represents an IgE-binding epitope"
                                                                                                Birch tree pollen allergen; P14 protein; pollinosis; profilin; in vitro diagnosis; antigenicity; poly L-proline; affinity.
                                                                                                                                                                                                                                                                                                                                                (BIOM-) BIOMAY BIOTECHNIK PRODN & HANDELS GMBH.
                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                             94AT-00000740.
                                                                                                                                                                                                                                                                                                                      94AT-00000740.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 4; 38pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.2%;
                                  (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                        Birch pollen P14 allergen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||| :||:|
HLGGIKYMV 76
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N-PSDB; AAQ89191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 HLGNVKYLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 133 AA;
                                                                                                                                      Betula pendula
                                                                                                                                                                                                                                                                                                                                                                                                                                         pollen extract
                                                                                                                                                                                                                                                                                             13-AUG-1990;
                                                                                                                                                                                                                                                                                                                      13-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-SEP-1999
                                 16-OCT-2003
09-NOV-1995
                                                                                                                                                                                                                                           AT9400740-A.
                                                                                                                                                                                                                                                                    15-FEB-1995
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          AAR71926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89
                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant DNA encoding polypeptide with epitope(s) of P14 allergens - for treatment and diagnosis of pollen or food allergy, and for purificn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pettenburg K, Breitenbac M, Kraft D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                    Gaps
                                                                                                                                                                                                                                                                                 Epitopes; pollen; food allergy; IgE antibodies; hyposensitisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.2%; Score 39; DB 2; Length 133; 66.7%; Pred. No. 10; ive 2; Mismatches 1; Indels
          Length 123
                                    1; Indels
          DB 4;
                    9.3;
                                  2; Mismatches
         Score 39;
Pred. No. 9
                                                                                                                                                  AAR22261 standard; protein; 133 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 4; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duchene M,
                                                                                                                                                                                                                                                                                                                                                                                    91WO-EP001513
        81.2%;
                                                                                                                                                                                                                                                                                                                                                                                                            90AT-00001685
91US-00683832
                                                                                                                                                                                                                                                                                                                                                                                                                                                   BIOM- BIOMAY BIOTECH PROD
                                                                                                                                                                                                    (revised)
(revised)
(first entry)
                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 66.7
es 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Uche, Duch
Scheiner O;
                                                                         ||| :||:|
58 HLGGIKYMV 66
                                                                                                                                                                                                                                                       P14 allergen of birch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 HLGNVKYLV 9
                                                           1 HLGNVKYLV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1992-096895/12.
                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of P14 allergens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAQ22352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 133 AA;
                                                                                                                                                                                                                                                                                                          Betula pendula,
                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-1991;
                                                                                                                                                                                                   24-OCT-2003
25-MAR-2003
09-JUL-1992
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                                                                                                                                                                                                                                                                                                                                    WO9203551-A
                                                                                                                                                                                                                                                                                                                                                            05-MAR-1992
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Rumpold H,
                                                                                                                                                                            AAR22261;
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          Query Match
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Matches
                                                                                                                       RESULT 13
AAR22261
                                  Matches
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                                                                                                                                                                                                                                                                                                                                              Major histocompatibility complex; class II; desensitising; human; allergen; grass; tree; weed; pollen; fungi; mould; food; insect; sting; chiromidae; spider; mite; housefily; fruit fly; sheep blow fly; honeybee; screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat; cockroach; beetle; dog; horse; ow; pig; sheep; rabbit; rat; guinea pig; mice; gerbil; vaccine; treatment; prevention; hypersensitivity.
                                       Gaps
                                       .;
0
                                       1; Indels
                                                                                                                                                                                                                                                                                                             Betula sp. allergen 130975 Bet v 2 protein fragment.
Score 39; DB 2;
Pred. No. 10;
2; Mismatches 1
                                                                                                                                                                                                      AAY25650 standard; protein; 133 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Betula sp
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AAR71926 standard; protein; 133 AA.

RESULT 14 AAR71926 ID AAR71

||| :||:| HLGGIKYMV 76

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This invention describes a novel method of desensitizing a patient to a colypeptide allergen and comprises administering to the patient a peptide derived from the allergen where restriction to a MHC Class II molecule cossessed by the patient can be demonstrated for the peptide and the peptide is able to induce a late phase response in an individual who peptide is able to induce a late phase response in an individual who peptide is able to induce a late phase response in an individual who competitising patients to allergens present in e.g. grass, tree and weed desensitising patients to allergens present in e.g. grass, tree and weed including ragweed) pollens, fungi and moulds, foods, stinging insects, the chiromidae (non-biting midges), spiders and mites, housefly, fruit in constitution moultor beetle, mammals such as cat, dog, horse, cow, pig, sheep, rabbit, rat, guinea pig, mice or garbil. They can also be used to produce immunological vaccines which may be used to prevent and/or treat conditions involving hypersensitivity to allergens. This sequence
                                                                                                                                                                                                                                                                                                   Desensitizing patients to polypeptide allergens.
                                                                                                                                                                                     (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD
                                                                                                                                                                                                                                                                                                                                           Example 6; Page 69; 117pp; English
                                                                                        99WO-GB000080
                                                                                                                              98GB-00000445
98GB-00020474
                                                                                                                                                                                                                                                                     WPI; 1999-458255/38.
                                                                                                                                                                                                                             Larche M, Kay AB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 133 AA;
                                                                                          11-JAN-1999;
                                                                                                                                09-JAN-1998;
21-SEP-1998;
                    WO9934826-A1
                                                        15-JUL-1999.
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Gaps ; Query Match

81.2%; Score 39; DB 2; Length 133;
Best Local Similarity 66.7%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 1; Indels

1 HLGNVKYLV 9 |||:||:| 68 HLGGIKYMV 76

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Search completed: December 6, 2004, 15:26:06 Job time : 131 secs

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GenCore version 5.1.6
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US-10-042-202-17 1 KNKEKALII 9 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 seqs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 23Sep04:* geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aar87283 Plasmodiu	Ade79963 Plasmodiu	Aay03664 Amino aci	Aay03681 Amino aci			Abb47928 Listeria	ы		Ade79962 Plasmodiu	Abo68759 Pseudomon	Abp38607 Staphyloc	Adm87702 Human EST	Abm70065 Photorhab	Abo64995 Klebsiell	Adj66998 Human sec		Arabic	-	Abu51874 Helicobac	Abu40414 Protein e	Aag38716 Arabidops	Aag22006 Arabidops	Abu51129 Helicobac	Aag38715 Arabidops
ID	AAR87283	ADE79963	AAY03664	AAY03681	AAR05427	ADA48468	ABB47928	ABP40575	AAR87282	ADE79962	AB068759	ABP38607	ADM87702	ABM70065	ABO64995	ADJ66998	ADM87247	AAG15384	AAG15383	ABU51874	ABU40414	AAG38716	AAG22006	ABU51129	AAG38715
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Length	0	6	11	229	559	348	177	227	0	σ	224	467	102	171	181	303	369	440	459	119	137	142	142	159	164
% Query Match	100.0	100.0	100.0	100.0	100.0	92.9	90.5	83.3	81.0	81.0	81.0	81.0	78.6	78.6	78.6	78.6	78.6	78.6	78.6			76.2	76.2	76.2	76.2
Score	42	42	42	42	42	39	38	35	34	34	34	34	33	33	33	33	33	33	33	32	32	32	32	32	32
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AAG22005 ADC97603 AAV27941 AAAC22004 ABU50835 ABU50835 AAB51761 ABU51761 ABU51761 ABU513699 AAU30690 ABU17482	ABU21836 ABU51958 AAW14068 AAB46319 AAY35710
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ALIGNMENTS

AAR87283 standard; peptide; 9 AA. (first entry) 16-MAY-1996 AAR87283; RESULT 1 AAR87283

Plasmodium falciparum HLA-B8 restricted epitope tr43.

Thrombospondin-related anonymous protein; human leucocyte antigen; HLA; class 1; HLA-B8; epitope; malaria; vaccine; CTL induction; cytotoxic T lymphocyte; TRAP.

Plasmodium falciparum.

WO9526982-A2.

12-OCT-1995.

95WO-GB000737. 31-MAR-1995; 94GB-00006492. 31-MAR-1994;

(ISIS-) ISIS INNOVATION LTD.

Aidoo M, Allsopp CEM, Lalvani A, Plebanski M; Whittle HC; Hill AVS,

WPI; 1995-358584/46.

Plasmodium falciparum peptide(s) - useful in vaccine compositions for immunising against malaria.

Claim 1; Page 18; 23pp; English.

Cytotoxic T lymphocytes from malaria-exposed Gambian individuals with HLBA-BB showed significant lysis of a pool of the four peptides tr42, tr43, tr44 and tr45 (all derived from Plasmodium falciparum thrombospondin-related anonymous protein (TRAB). The peptides tr42 and tr43 (AAR87282 and AAR87283) bound to HLA-BB in the HLA assembly assay. Subsequently, the same CTL line showed specific lysis of tr42 only, while CTL from another adult showed specific lysis of the tr43 peptide, identifying tr42 and tr43 as overlapping HLA-BB restricted epitopes. These peptides will be useful in a malaria vaccine

Sequence 9 AA;

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The invention relates to methods and reagents for generating a protective
                                                                                                                     CD8+ T-cell; immune response; antigen; priming composition; CTL; epitope; cytotoxic T lymphocyte; boosting; poxvirus vector; PVV; pathogen; tumour; malaria; parasite; P. falciparum; viral; bacterial; parasitic; cancer; melanoma; HIV; breast; colon; vaccination.
                                                                             Amino acid sequence of the malaria (M) string CTL epitope Tr42/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Generating CD8-positive T cell response to target antigen using recombinant poxyirus - for treating or preventing malaria and HIV infection, also epitope strings from Plasmodium and HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NVS, Gilbert SC, Schneider J, Plebanski M;
Blanchard T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 38; Page 18; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  98WO-GB001681.
                                                                                                                                                                                                                                                                                                                                                                                                                          97GB-00011957.
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                                            (first entry)
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Hanke T, Smith GL, Blan
                                                                                                                                                                                                                                                Plasmodium falciparum
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Best Local Similarity
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                                            07-JUN-1999
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AAY03664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method of generating an immune response against a non-hepadnaviral antigen in a mammal by administering (to the mammal) at least 1 dose of a priming component comprising a recombinant hepatitie B core particle (rHEP) (which is a carrier for 1 or more non-hepadnaviral CD8+ T-cell epitopes of the antigen). The method may be supplemented by the use of a boosting stage comprising a non-replicating or replication-impaired recombinant poxvirus vector. The method is useful for generating an immune response against a non-hepadnaviral antigen in a mammal for treating or preventing cancer or malaria. This sequence
                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium epitope #19 for method to augment CD8+ T-cell immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mammal, useful for treating or preventing cancer or malaria, by administering a priming component comprising a recombinant hepatitis B core particle.
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                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 antimalarial; cytostatic; vaccine; immune response;
non-hepadnaviral antigen; hepatitis B core particle; CD8+ T-cell;
epitope; poxvirus vector; cancer; malaria; epitope.
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         Length 9;
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ilarity 100.0%; Pred. No. 1.70+06;
Conservative 0; Mismatches
         100.0%; Score 42; DB 2; I
100.0%; Pred. No. 1.7e+06;
                                                        0; Mismatches
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                                                                                                                                                                                                                                                            ADE79963 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                          9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KNKEKALII 9
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Matches 9; Conserv
                                                                                                       1 KNKEKALII
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              Query Match
Best Local Similarity
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                                                             Matches
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ADE79963
ADE79963
ANC ADE ANC ADEA ANC ADE ANC ADEA ANC AD
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The invention relates to methods and teagents to generating a provedive CC CDB+ T-cell lammer seponse against at least one target antigen. The kits of the invention comprises (i) as priming composition, a source of one or cof the invention comprises (ii) as boosting composition a source of one or cof cof the invention at carrier and (ii) as boosting composition a source of CTL antigen, plus a carrier and (ii) as boosting composition a source of CTL epitopes, with at least one CTL epitope the same as used in (i), with this source being a non-replicating or replication-impaired recombinant this source being a non-replicating or replication-impaired recombinant (i) is a viral vector, then the vector in (ii) is from a different virus. (i) is a viral vector, then the vector in (ii) is from a different virus. CT the kits are used to generate an immune response (prophylactic or therapeutic) against pathogens or tumours, specifically against malaria (i) therapeutic) against pathogens or tumours, specifically against malaria. CT viral or parasitic pathogens. The kits are also used for protective or viral or parasitic pathogens. The kits are also used for protective consposition wherever a strong CDB+ response is protective. The boosting composition may be used alone to boost a naturally primed response against malaria. The specified PVV provide an excellent booster effect, better than that protection against sporozoite challenge. Also PVV are safer to use than wild-type virus. Sequences AAY03661-680 represent CTL peptide epitopes of the malaria (M) string
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AC AAY0
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AAY03664 standard; peptide; 11 AA.

RESULT 3
AAY03664
ID AAY0:

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The invention relates to methods and reagents for generating a protective CD8+ T-cell immune response against at least one target antigen. The kits CD8+ T-cell immune response against at least one target antigen. The kits or the invention comprehence of the perpetual invention comprehence of one or more CD8+ T-cell [cytotoxic T lymphocytes-(CTL)] epitopes of the target antigen, plus a carrier and (ii) as boosting composition a source of CTL epitopes, with at least one CTL epitope the same as used in (i), with this source being a non-replicating or replication-impaired recombinant poxylivus vector (PVV) plus a carrier. If the source of CTL epitopes in (i) is a viral vector, then the vector in (ii) is from a different virus. The kits are used to generate an immune response (prophylactic or therapeutic) against pathogens or tumours, specifically against malaria parasites such as P. falciparum, or HIV, and also many other bacterial, viral or parasitic pathogens. The kits are also used for protective cresponse against melanoma and cancer of breast or colon, and generally wherever a strong CD8+ response is protective. The boosting composition may be used alone to boost a naturally primed response against malaria. The specified PVV provide an excellent booster effect, better than that the mid-type poxvirus, resulting in complete rather than partial primed response.
                                                                                              CD8+ T-cell; immune response; antigen; priming composition; CTL; epitope; cytotoxic T lymphocyte; boosting; poxvirus vector; PVV; pathogen; tumour; malaria; parasite; P. falciparum; viral; bacterial; parasitic; cancer; melanoma; HIV; breast; colon; vaccination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Generating CD8-positive T cell response to target antigen using recombinant poxvirus - for treating or preventing malaria and HIV infection, also epitope strings from Plasmodium and HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 42; DB 2; Length 229; 100.0%; Pred. No. 4.6; ive 0; Mismatches 0; Indels
                                                        Amino acid sequence of the malaria (M) string CTL epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mcmichael AJ, Hill AVS, Gilbert SC,
Hanke T, Smith GL, Blanchard T;
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                    07-JUN-1999 (first entry)
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                                                                                                                                                                                                Plasmodium falciparum
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Best Local Similarity
Matches 9; Conser
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25-MAR-2003
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AAR05427
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Schneider J, Plebanski M;

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The CS protein is produced during the merozoite stage of the malaria parasite. The CS-related protein can be used to produce vaccines. The antibodies can be used for purificn. of the polypeptides. The vector may be a recombinant virus, esp. baculovirus or the peptide can be chemically prepared. Fragments of the peptide preferably contain a conserved sequence, egresidues 244 to 291 and more particularly a polypeptide selected from the following group: A) WDEWSPCSVTCGKGTRSRKR B) WDEWSPCSVTCGKGTR C) EWSPCTYTCGKG D) PCSVTCGKG B) WSPCSVTCG See also AAQ02049. (Updated on 25-MAR-2003 to correct P1 field.) (Updated on 24-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                      DNA cloned from Plasmodium falciparum - used to prepare polypeptide(s) used in vaccines for persons suffering from or at risk from malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease resistance; pathogen tolerance; plant pathogen; plant; rice.
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                                                         88.
                                                      Plasmodium falciparum; malaria; vaccine;
                           Circumsporozoite (CS)-related protein.
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                                                                                  Plasmodium falciparum; T.9/96
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                                                                                                                                                                    89WO-GB000895
                                                                                                                                                                                               88GB-00019209
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26-JUL-1990 (first entry)
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                                                                                                                                                                                                                                                                                             WPI; 1990-083478/11.
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ADA48468
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Gaps

SA, Moughamer T;), Zhu T;

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The invention relates to a novel isolated polynucleotide comprising a plant nucleotide sequence having an open reading frame that encodes a polypeptide associated with disease resistance or its fragment having substantially the same activity as the full-length polypeptide. The polynucleotide of the invention is useful for conferring resistance or tolerance to a plant pathogen. The present sequence represents a protein conferring disease resistance used in the invention.
                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide comprising a plant nucleotide sequence having an open reading frame that encodes a polypeptide associated with disease resistance, useful for conferring resistance or tolerance to a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P; Duseurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P; Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Borland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquer F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.9%; Score 39; DB 6; Length 348; 77.8%; Pred. No. 26; ive 2; Mismatches 0; Indels
                                                                                                                                                                     , Goff SA,
Ricke D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 10; SEQ ID NO 538; 299pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Listeria monocytogenes protein #632
                                                                                                                                                                     Glazebrook J, Briggs S, Cooper B,
Katagiri F, Kreps J, Provart N, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB47928 standard; protein; 177 AA.
                                                                                                     (SYGN ) SYNGENTA PARTICIPATIONS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-APR-2000; 2000FR-00004629
26-SEP-2001; 2001US-0352277P.
22-MAR-2002; 2002US-0366535P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 77.8
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KNKEKALLV 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KNKEKALII 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-010914/01
                                                                                                                                                                                                                                                                          WPI; 2003-184052/18.
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                                                                                                                                                                                                                                                                                                             N-PSDB; ADA48467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 348 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200177335-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB47928

AC ABB4

AC ABB6

AC
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The present invention relates to the genome sequence of Listeria

common cytogenes EGD-e (see ABA03041). The genome sequence and fragments of

to are useful for selecting probes and primers for detecting genes in L.

comportogenes and related organisms, and for studying genetic

monocytogenes and related organisms, and for studying genetic

composed by the genome sequence of the present invention. Proteins

composed by the genome sequence are useful for raising specific

antibodies, identification of L. monocytogenes and related organisms, and

composed from the genome sequence are useful for raising specific

antibodies, identification of L. monocytogenes and related organisms, and

compounds that regulate gene expression and cell replication

compositions that regulate gene expression and cell replication

compositions for the treatment or prevention of infections by L.

compositions for the treatment or prevention of infections by L.

compositions and related organisms. Note: The sequence data for this

compositions forms part of the printed specification, but was obtained

compositions format directly from WIPO at

compos
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Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated nucleic acid encoding a Staphylococcus epidermis
polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Length 177;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB 5; Pred. No. 21; 0; Mismatches
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                                                                                                 Claim 6; SEQ ID NO 633; 192pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP40575 standard; protein; 227 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.5%;
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97US-0064964P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus epidermidis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibacterial; gene therapy
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Best Local Similarity 88.9
Matches 8; Conservative
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N-PSDB; ABN93120.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KNKEKALII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 177 AA;
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08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-AUG-1998;
                                                       polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUL-2002
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Gaps

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given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cions. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
  (ORF) nucleic acid sequences which encode the amino acid sequences
     frame
888888888888888
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Sequence 227 AA;

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Gaps
                        ;
0
         Length 227;
                        0; Indels
        Score 35; DB 5;
Pred. No. 1e+02;
2; Mismatches
      83.3%;
Query Match
Best Local Similarity 75.vv,
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RESULT 9 AAR87282

AAR87282 standard; peptide; 9 AA. AAR87282;

16-MAY-1996 (first entry)

Plasmodium falciparum HLA-B8 restricted epitope tr42.

Thrombospondin-related anonymous protein; human leucocyte antigen; HLA; class 1; HLA-B8; epitope; malaria; vaccine; CTL induction; cytotoxic T lymphocyte; TRAP.

Plasmodium falciparum

WO9526982-A2

12-OCT-1995

95WO-GB000737 31-MAR-1995; 94GB-00006492 31-MAR-1994;

(ISIS-) ISIS INNOVATION LTD

Lalvani A, Plebanski Aidoo M, Allsopp CEM, Whittle HC; Hill AVS,

WPI; 1995-358584/46.

Plasmodium falciparum peptide(s) - useful in vaccine compositions for immunising against malaria.

Claim 1; Page 18; 23pp; English.

Cytotoxic T lymphocytes from malaria-exposed Gambian individuals with HLA-B8 showed significant lysis of a pool of the four peptides tr42, tr43, tr44 and tr44 and tr46 flal derived from Plasmodium falciparum thrombospondin-related anonymous protein (TRAP)). The peptides tr42 and tr43 (AAR87282 and AAR87283) bound to HLA-B8 in the HLA assenbly assay. Subsequently, the same CTL line showed specific lysis of tr42 only, while CTL from another adult showed specific lysis of the tr43 peptide, identifying tr42 and tr43 as overlapping HLA-B8 restricted epitopes. These peptides will be useful in a malaria vaccine

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Query Match 81.0%; Score 34; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 1.7e+06; Matches 7; Conservative 0; Mismatches 0; Indels
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ABO68759 standard; protein; 224 AA.

RESULT 11

AB068759

3 KNKEKAL

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29-JUL-2004 (first entry)

ABO68759;

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The invention relates to a method of generating an immune response against a non-hepadnaviral antigen in a mammal by administering (to the mammal) at least 1 dose of a priming component comprising a recombinant hepatitis B core particle (*HEP) (which is a carrier for 1 or more non-hepadnaviral CD8+ T-cell epitopes of the antigen). The method may be supplemented by the use of a boosting stage comprising a non-replicating or replication-impaired recombinant poxvirus vector. The method is useful for generating an immune response against a non-hepadnaviral antigen in a mammal for treating or preventing cancer or malaria. This sequence represents a peptide epitope from Plasmodium the causative agent for
                                                                                                                                                                                                               Plasmodium epitope #18 for method to augment CD8+ T-cell immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               non-hepadnaviral antigen in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Generating an immune response against a non-hepadnaviral antigen in a mammal, useful for treating or preventing cancer or malaria, by administering a priming component comprising a recombinant hepatitis core particle.
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                                                                                                                                                                                                                                                             CD8+ T-cell;
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                                                                                                                                                                                                                                            vaccine, immune response;
hepatitis B core particle;
cancer; malaria; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 57; SEQ ID NO 18; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYNY-) UNIV NEW YORK MEDICAL CENT
                                                                                                             ADE79962 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                               07-FEB-2003; 2003WO-US003897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                08-FEB-2002; 2002US-0354963P
                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                antimalarial; cytostatic;
non-hepadnaviral antigen;
                                                                                                                                                                                                                                                                               epitope; poxvirus vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birkett AJ;
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                    3 KNKEKAL
KNKEKAL
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                                                                                                                                                                               29-JAN-2004
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                                                                                                                                              ADE79962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   malaria.
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ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have mathbacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis ilfe cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       respiratory; cytostatic; antiarthritic; antiinflammatory; gastrointestinal; antibacterial; immunosuppressive; antidiabetic; antirheumatic; gene therapy; molecular weight marker; chromosome tag; genetic fingerprinting; nutritional supplement; cancer; inflammatory condition; arthritis; inflammatory bowel disease; crohn's disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1; graft versus host disease; human; expressed sequence tag; EST.
                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
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66.7%; Pred. No. 3.38+02;
ive 2; Mismatches 1; Indel8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human EST derived amino acid sequence SEQ ID NO:795.
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                                                                                                                                                                                       (GENO-) GENOME THERAPEUTICS CORP.
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28-MAR-2002; 2002US-00112944.
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                                              98US-00134001
                                                                                                     97US-0055779P.
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                                                                                                                                                                                                                                              Bush D;
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N-PSDB; ABN91152.
                                                                                                                                                                                                                                                 Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NUVE-) NUVELO INC.
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 467 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2004009834-A2
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                                                 13-AUG-1998;
                                                                                                        14-AUG-1997;
08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JUN-2004
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30-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to Pseudomonas aeruginosa polypeptides and the polymicleotides encoding them. The sequences are useful in diagnosis and therepay of pathological conditions, as molecular targets for diagnosities, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of pseudomonas species using biochip technology. Sequences ABOG 7826-CABOR 1994 For this parent did not form part of the printed sequence data for this parent did not form part of the printed sequence data for this parent did not form part of the printed sequence are all the printed sequences are all the printed sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                       Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.0%; Score 34; DB 7; Length 224; 75.0%; Pred. No. 1.6e+02; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 17505; 455pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deloughery C,
     Pseudomonas aeruginosa polypeptide #934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP38607 standard; protein; 467 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                       (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            segdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                      98US-0074788P
98US-0094190P
                                                                                                                                                                                                                                                                                 99US-00252991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                       Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 KNKQKALV 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-615309/58.
N-PSDB; ABD02330.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rubenfield MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US6380370-B1
                                                                                                                                                                                                                                                                                       18-FEB-1999;
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Gaps

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Length 467;

Wang J;

Tang YT,

RESULT 12 ABP38607

Matches

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The present invention describes an isolated polymucleotide (1): (a)

Comprising a nucleotide sequence selected from SEQ ID NO:1-24; or (b)

which encodes a polypeptide with biological activity, where the

CC polymucleotide hybridises to (1) under stringent hybridisation conditions

Or has greater than 99% sequence identity with (1). (1) has respiratory,

Cytostatic, antiarthritic, antiinflammatory, gastrointestinal,

CC danibacterial, immunosuppressive, antidiabetic and antirheumatic

CC antibacterial, immunosuppressive, antidiabetic and antirheumatic

CC activities, and can be used in gene therapy. (1) can be used for

CC dentaring polymucleotides encoding chimeric or fusion proteins and

CC express recombinant protein for analysis, characterisation or therapeutic

CC express recombinant protein for analysis, characterisation or therapeutic

CC express recombinant protein for analysis, characterisation or therapeutic

CC express recombinant protein for analysis, characterisation or therapeutic

CC express recombinant protein for analysis, characterisation or therapeutic

CC express recombinant protein for analysis, characterisation or therapeutic

CC express recombinant protein for analysis, characterisation or therapeutic

CC express recombinant protein for analysis, characterisation to derive PCR

CC frames for genetic fingerprinting; as probe to subtract-out known

CC dentify potential genetic disorders; as probe to subtract-out known

CC dentify potential genetic fingerprinting; as a probe to subtract-out known

CC dentify potential genetic fingerprinting; as a probe to subtract-out known

CC dentify and making oligomers for attendment to a gene chip or other

CC protein antibodies using DNA immunisation techniques; and as an antigen

CC raise anti-bodies and polypeptides can also be used as autritional source

CC corpositions are useful for promoting better or faster closure of non-

CC contositions are useful for promoting better or faster closure of nor-

CC contositions are useful on an and probe to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage. The compositions can also be used to treat tillammatory conditions (e.g. arthritis, inflammatory bowel disease or Crohn's disease), sepsis, rheumatorid arthritis, diabetes mellitus type 1 or graft versus host disease. The present sequence represents an expressed sequence tag (EST) derived amino acid sequence from the present
                                                                                                                                         New isolated polynucleotides and polypeptides, useful for treating, e.g. cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease, Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention. N.B. The sequences for this patent were obtained from the USPTO web site from an equivalent US patent US20040048249A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protection or regeneration and treatment of lung or liver fibrosis,
                                                                                                                                                                                                                                                                                                                                                     The present invention describes an isolated polynucleotide (I): (a)
Zhao QA, Wang Z;
                                                                                                                                                                                                                                                                                              Example 2; SEQ ID NO 795; 591pp; English
   Wang D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.6%;
Ghosh MJ,
                                                         2004-143291/14
                                                                                                                                                                                                                                    versus host disease.
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Best Local Similarity
                                                                                     N-PSDB; ADM87484
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Wehrman T,
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Gaps
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Score 33; DB 8; Length 102;
Pred. No. 1.1e+02;
2; Mismatches 0; Indels
                               6; Conservative
                                                            2 NKEKALII 9
                               Matches
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ABM70065 standard; protein; 171 AA. (first entry) ||||||||| 80 NKEKAIIL 87 20-NOV-2003 ABM70065; RESULT 14 셤

Antibacterial; fungicide; insecticide; polymorphism; genetic analysis; Photorhabdus luminescens protein sequence #3162.

The invention relates to the isolation of genes and their encoded proteins from Photorhabdus luminescens. The isolated sequences are sources of probes and primers for detecting the genome of P. luminescens and related species; to study polymorphisms, for gene analysis and for detection/amplification of the genes. Antibodies (Ab) raised against the polymorphisms, for gene analysis and for detection/amplification of the genes are used for detection/identification of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that carry a gene-containing vector are used to select compounds that modulate, regulate, induce or inhibit expression of the genes in plants, modulate, regulate, induce or inhibit expression of the genes in plants, response or sensitivity to toxins and antibiotics production of the proteins, particularly toxins and crecambinant production of the proteins, particularly toxins and cantibacterials useful as insecticides, particularly toxins and fungicides. The genes, proteins, vectors containing the genes and Ab are also useful care sensitive to P. luminescens and infection by bacteria or fungi that are sensitive to P. luminescens and the proteins are as virulence factors and for identifying targets of human diseases for which P. ö detection; food; gene expression; plant; animal; microorganism; toxin; antibiotic; biopesticide; virulence factor; disease model; plague; luminescens is a model (particularly plague and whooping cough). This sequence represents one of the isolated P. luminescens proteins Genomic sequence of Photorhabdus luminescens and encoded polypeptides useful e.g. as therapeutic antimicrobials and agricultural pesticides Gaps Danchin A; ö 78.6%; Score 33; DB 6; Length 171; 75.0%; Pred. No. 1.9e+02; ive 2; Mismatches 0; Indels Kunst F, Frangeul L, Claim 2; SEQ ID NO 3162; 1205pp; French. Taourit S, Glaser P, RECH SCI 07-FEB-2002; 2002WO-IB003040. 07-FEB-2001; 2001FR-00001659. 6; Conservative Photorhabdus luminescens, CNRS) CNRS CENT NAT ||||||:: 136 NKEKALLL 143 WPI; 2003-148459/14. 2 NKEKALII 9 Best Local Similarity Sequence 171 AA; whooping cough. WO200294867-A2. Duchaud E, Ta Buchrieser C; INSP) INST 28-NOV-2002 Query Match RESULT 15 ABO64995 Matches පු ð

Recombinant expression vector; transcription regulatory element; Klebsiella pneumoniae protein; antibacterial; Vaccine. Klebsiella pneumoniae polypeptide segid 11512. ABO64995 standard; protein; 181 AA. (first entry) 29-JUL-2004 AB064995;

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0; Gaps

Search completed: December 6, 2004, 15:26:09 Job time : 122 secs 4024, Ap 3710, Ap 1, Appli 15896, A

7854, Ap 4220, Ap 15210, A 1131, Ap 17527, A 6, Appli

Sequence Seq

6, Appli 57870, A 9, Appli 2, Appli 389, App

2711, Ap 42238, A

Sequence

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GENERAL INVERGRATION:
GENERAL INVERGRATION:
APPLICANT: Hill, Adrian V.S.
APPLICANT: Gilbert, Sarah C.
APPLICANT: Gilbert, Sarah C.
APPLICANT: Schneider, Jorg
APPLICANT: Schneider, Jorg
APPLICANT: Sath, Geoffrey L.
APPLICANT: Blanchard, Tom
TITLE OF INVENTION: Methods and Reagents for Vaccination
TITLE OF INVENTION: Mobil Generate A CD8 T Cell Immune Response
FILE REFERENCE: 2307.1000-0009
FILE REFERENCE: 2307.1000-0009
FILE REFERENCE: 1999-12-09
FRIOR APPLICATION NUMBER: US/09/454,204A
FRIOR APPLICATION NUMBER: PCT/GB98/01681
FRIOR PLILNG DATE: 1998-06-09
NUMBER OF SEQ ID NOS: 78
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: II
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100.0%; Pred. No. 0.043;
ive 0; Mismatches 0; Indels
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                                                        US-09-248-796A-15896
US-09-248-796A-15896
US-09-107-523A-4220
US-09-108-452A-1131
US-09-248-796A-17527
US-08-723A-6
US-09-221-114-6
US-09-270-767-57870
US-09-270-767-57870
US-09-155-920-2
US-09-155-920-2
US-09-158-927A-389
US-09-158-927A-389
US-09-158-927A-389
US-09-158-927A-389
US-09-158-927A-389
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US-09-158-927A-389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 41, Application US/09454204A, Patent No. 6663871; GENERAL INFORMATION: APPLICANT: Hill, Adrian V.S. APPLICANT: Glibert, Sarah C. APPLICANT: Schneider, Jorg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/09454204A Patent No. 6663871
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Best Local Similarity 100.
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
US-09-454-204A-41
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  FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 41, Appl
Sequence 14, Appl
Sequence 16240, Ap
Sequence 17505, A
Sequence 3368, A
Sequence 3452, Ap
Sequence 7230, Ap
Sequence 7230, Appl
Sequence 5, Appli
Sequence 18964, A
Sequence 18964, A
Sequence 18964, A
Sequence 17, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 10, Appli
Sequence 20, Appli
Sequence 20, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 22, Appli
Sequence 23, Appli
Sequence 24, Appli
Sequence 27, Appli
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Sequence 4272, Ap
Sequence 25586, A
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                                                                                                                                               December 6, 2004, 15:19:38 ; Search time 27.5 Seconds (without alignments) 21.704 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
                  GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-454-204A-41
US-09-454-204A-41
US-09-134-001C-5420
US-09-248-796A-16240
US-09-248-796A-16240
US-09-270-767-35368
US-09-270-767-50585
US-09-134-001C-3452
US-09-134-001C-3452
US-09-134-001C-3452
US-09-248-796A-18964
US-09-248-796A-18964
US-09-134-000C-6570
US-09-134-00C-6570
US-09-134-000C-6570
US-09-134-000C-6570
US-09-134-00C-6570
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                                                                                                                                                                                                                                                                                                                                                                                                        478139 seqs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                         - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Issued Patents AA:*
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Maximum DB seq length: 200000000
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Match Length
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2 6 4 6 6

Database

Score

Result

Scoring table:

Searched:

Perfect score:

Sequence:

OM protein

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Gaps

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Length 11;

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; ANTI-SENSE:
US-08-313-288B-14
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                  APPLICANT: Hanke, Tomas
APPLICANT: Hanke, Tomas
APPLICANT: Smith, Geoffrey L.
APPLICANT: Smith, Geoffrey L.
APPLICANT: Smith, Geoffrey L.
TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response;
TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response;
TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response;
CURRENT APPLICATION NUMBER: US/09/454,204A
CURRENT FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-06-09
PRIOR FILING DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41
LENGTH: 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 42; DB 4; Length 229;
Best Local Similarity 100.0%; Pred. No. 0.9;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/08313288B
Patent No. 5750502
GENERAL INFORMATION:
APPLICANT: Jessell, Thomas M. and Avihu Klar
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,288B
FILING DATE: January 5, 1995
ATTONEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Complete Epitope of Malaria String
US-09-454-204A-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1185 Avenue of the Americas CITY: New York COUNTRY: USA YORK
  Plebanski, Magdalena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 559 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 KNKEKALII 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: li
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US-08-313-288B-14
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Sequence 16240, Application US/09248796A

Sequence 16240, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLBIC ACID AND THERAPEUTICS

TITLE OF INVENTION: NUCLBIC ACID AND THERAPEUTICS

FILE REFRENCE: 107196.132

CURRENT FILING DATE: 1999-02-12

PRIOR PELICATION NUMBER: US 60/074,725

PRIOR PILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 16240

LENGTH: 198
                                                                                                                                                                                                                                                   Sequence 5420, Application US/09134001C

Patent No. 6380370

Patent Application Number: US/09/134,001C

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR PAPICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR PILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 5420
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100.0%; Score 42; DB 1; Length 559; 100.0%; Pred. No. 2.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35; DB 3; Length 227;
Pred. No. 21;
2; Mismatches 0; Indels
                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Staphylococcus epidermidis US-09-134-001C-5420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Candida albicans
Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                      109 KNKEKALII 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 KNKEKSAII 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KNKEKALII 9
                                                                                              1 KNKEKALII 9
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11 NKEKALVV 18
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                                                                                                                                                                                                                   RESULT 4
US-09-134-001C-5420
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Gaps

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Patent No. 6380370

Batent No. 6380370

GENERAL INPORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-01-08

PRIOR FILING DATE: 1997-01-08

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 3452

LENGT: APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

SEQ ID NO 3452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11512. Application US/09489039A

PITTLE OF INVERVION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVERVION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVERVION: NUCLEIC ACID AND AMINO ACID SEQUENCES

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 1999-01-29

PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33; DB 4; Length 181;
Pred. No. 41;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.0%; Score 34; DB 3; Length 467; 66.7%; Pred. No. 68;
                                                                                                                                                                                  4; Length 299;
                                                                                                                                                                                  Score 34; DB
Pred. No. 43;
                                                                                  FEATURE:
; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-50585
                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Staphylococcus epidermidis
                LENGTH: 299
TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11512
                                                                                                                                                                                Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative 7
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SEQ ID NO 11512
LENGTH: 181
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Best Local Similarity 66.7
Matches 6; Conservative
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142 KNQEQALII 150
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US-09-134-001C-3452
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SEQ ID NO 50585
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                                           Sequence 17505, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
PAPLICATION:
HOUSELD NOT MACE JUBBER ALL
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

LENGTH: 224
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 35568
LENGTH: 299
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US-09-270-767-50585
US-09-270-767-50585, Application US/09270767
; Sequence 50585, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;
; FILE REFERENCE: File Reference: 7326-094
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB 4; Length 224;
Pred. No. 32;
2; Mismatches 0; Indels
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Pred. No. 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-35368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.0%;
75.0%;
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Best Local Similarity 77.0
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                                         US-09-252-991A-17505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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us-08-476-515A-5
; Sequence 5, Application US/08476515A
; Sequence 5, Application US/08476515A
; Patent No. 6239270
; GENERAL INFORMATION:
    APPLICANT: Akerstrom, Goran
APPLICANT: Rask, Lars
    APPLICANT: Rask, Lars
    APPLICANT: Morse, Clarence C.
    APPLICANT: Murray, Edward M.
    APPLICANT: Hjalm, Goran
    TITLE OF INVENTION: Thereof and DNA Encoding Same
    NUMBER OF SEQUENCES: 84
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Martin g...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 269 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :|||| |::
166 ENKEKVLVV 174
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                                                                                                                           Sequence 7230, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEPHONE: (781)893-5077
INFORMATION FOR SEQ ID NO: 7230:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature;
COCATION: (B) LÖCATION 1...166;
SEQUENCE DESCRIPTION: SEQ ID NO: 7230:
US-09-107-532A-7230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: CC/ROM SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08652877
Patent No. 6187548
GENERAL INFORMATION:
APPLICANT: ARErstrom, Goran
APPLICANT: Jullin, Claes
APPLICANT: Rask, Lars
APPLICANT: Crumley, Gregg R.
                                                                                                                                                                                                                                                                                                                                               CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 KNKEEAFLI 41
||| |||::
6 KNKAKALVL 14
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                                                                                       RESULT 11
US-09-107-532A-7230
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US-08-652-877-5
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Gaps

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APPLICANT: Morse, Clarence C.
APPLICANT: Murray, Edward M.
APPLICANT: Hjalm, Goran
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
TITLE OF INVENTION: Thereof and DNA Encoding Same
VUMBER OF SEQUENCES: 106
CORRESSONDENCES.
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Rd., 3C43
CITY: Collegeville
STREET: DA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 32; DB 3; Length 269;
Pred. No. 96;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15203
FILING DATE: 22-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,314
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,314
FILING DATE: O'-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: SAVLEXY, MARTÍN
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: 29,699
REFERENCE/DOCKET NUMBER: 29,699
REFERENCE/DOCKET NUMBER: A1355E-US
TELEPHONE: 610-454-3806
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE: CHARACTERISTICS:
                                                                                                                                                                                                                                                              CITY: Collegeville
STATE: PA
COUNTE: PA
ZIP: 19426-0107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macincoh
OPERATING SYSTEM: System 7.5.1
SOFTWARE: Word 6.0 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,877
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Gaps
      Gaps
                                                                                                                                                                                              Sequence 7, Application US/08671757A
Patent No. 6476213
GENERAL INFORMATION:
APPLICANT: Suerbaum, Sebastian
TITLE OF INVENTION: Cloning and Characterization Production
of Aflagellate Strains
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0
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CITY: Washington
COUNTR: D.C.
COUNTR: D.C.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATION NUMBER: US/08/671,757A
FILING DATE: 16-Aug-2001
CLASSIFICATION: «Unknown»
ATTORNY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 75.2%; Score 32; DB 4; Length 732; Best Local Similarity 75.0%; Pred. No. 2.6e+02; Matches 6; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
Dunner
      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERRNCE/DOCKET NUMBER: 02356.0073-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
TELEFRAX: (202) 408-4400
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    2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) MOLECULE TYPE: peptide
) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-671-757A-7
                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 732 amino acids
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
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    6; Conservative
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                                                                       ||||:||:
417 NKEKSLIL 424
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503 KNKEEAII 510
                                              2 NKEKALII 9
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    Matches
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Keith Meinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196-132
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR PELING DATE: 1998-02-13
PRIOR PELICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18964
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Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;
                                                                                                COMPUTER: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: I POPPY disk

COMPUTER: Compaq PC

OPERATING SYSTEM: Windows 95

SOFTWARE: Word 7.0 (Patentin)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/476,515A

FILING DATE: 07-UNN-1995

FILING DATE: 23-NOV-1994

PRIOR APPLICATION DATA:

FILING DATE: 23-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/SE94/00483

FILING DATE: 24-MAY-1994

APPLICATION NUMBER: SE 9301764-8

FILING DATE: 24-MAY-1994

APPLICATION NUMBER: SE 9301764-8

FILING DATE: 24-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: SAVICZKY, MARTÍN

REGISTRAFION NUMBER: 25-699

DEFEDERATION NUMBER: 25-699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: A1355D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-454-3816
TELEFAX: 610-454-3808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 610-454-3808
INPORMATION POR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: amino acid
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Best Local Similarity 55.6
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|||| |::
166 ENKEKVLVV 174
                                           Collegeville
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Best Local Similarity
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US-09-248-796A-18964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-476-515A-5
                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM:
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
               Copyright
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OM protein - protein search, using sw model

6, 2004, 15:18:43; Search time 23.5 Seconds (without alignments) 36.849 Million cell updates/sec December Run on:

US-10-042-202-17 1 KNKEKALII 9 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:* Database :

piri:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	thrombospondin-rel	sporozoite surface	modulates DNA topo	flaR protein - Lis	UDP-N-acetylmuramo	conserved hypothet	hypothetical prote	PP-loop superfamil	hypothetical prote		ate o-ac	A/G-specific adeni	hypothetical prote	unknown protein, 8	translation releas	conserved hypothet	hypothetical prote	hypothetical prote	ATP-dependent DNA	hypothetical prote			-	translation releas			chain		nift w
SUMMARIES	ΩΙ	S04531	A46283	AD1251	S70846	A84956	F70406	D84676	C97345	T31105	837351	A83201	D84994	855630	F96570	S76448	B99952	D84636	AD1731	AD2237	A64465	T47547	T43754	H81536	E64529	F71977	S55437	G84121	972	B72130
	рв	2	~	7	~	~	~	~	~	~	~	~	~	N	~	ч	~	~	7	(7	7	N	~	~	~	~	Н	~	~	0
	Length	559	574	177	177	497	468	174	222	4919	216	216	350	154	320	372	443	465	518	698	1005	164	232	241	352	352	356	356	359	456
d	Query Match		100.0	0	90.5	8	ď.	c	m	83.3	81.0	81.0	81.0	78.6	78.6	78.6	78.6	78.6	78.6	78.6	78.6	76.2	76.2	v	ဖ	v	76.2	ဖ	76.2	76.2
	Score	42	42	38	38	37		35						33				33	33		33	32		32	32	32	32	32	32	32
	Result No.		7	n	4	ស	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote flagellar biosynth flagellar biosynth hypothetical prote hypothetical prote hypothetical prote glycoprotein GP330 dominant autoantig hypothetical 527K gg330 protein prec hypothetical prote hypothetical prote hypothetical 14.5K CPSD/CARA conserve CPSD/CARA conserve probable exported	hypothetical prote
2 A64650 2 E71937 2 B86492 2 B86492 2 B33363 2 A33363 2 A33363 2 S57908 2 T5737 2 JQ1539 2 E97276 2 B97276 2 B97276	2 D91261
561 733 733 774 774 774 911 972 811 811 1126 227 227 229	229
88888777777777777777777777777777777777	73.8
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	31
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## ALIGNMENTS

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Unionbospondin-related protein TRAP - malaria parasite (Plasmodium falciparum)
N.Alternate names: thrombospondin-related anonymous protein
C.Species: Plasmodium falciparumm.
C.Species: Plasmodium falciparumm.
C.Species: Plasmodium falciparumm.
C.Species: Plasmodium falciparumm.
C.Species: O7-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C.Accession: S04531
R.Robson, K.J.H.; Hall, J.R.S.; Jennings, M.W.; Harris, T.J.R.; Marsh, K.; Newbold, C.I.;
Nature 335, 79-82, 1988
A.Title: A highly conserved amino-acid sequence in thrombospondin, properdin and in prote
A.Reference number: S04531
A.Molecule type: DNA
A.Rocession: S04531
A.Molecule type: DNA
A.Rocession: L559 cROB-
A.Cross-references: UNIPROT:P16893; EMBL:X13022; NID:g9977; PID:g9978
F;240-287/Domain: thrombospondin type 1 repeat homology <THR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Best Local Similarity 100.
Matches 9; Conservative
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S04531
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sporozoite surface protein 2 - malaria parasite (Plasmodium falciparum) (strain NF54)
N.Alternate names: thrombospondin-related anonymous protein (TRAP)
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Accession: A46283
R;Rogers, W.O.; Malik, A.; Mellouk, S.; Nakamura, K.; Rogers, M.D.; Szarfman, A.; Gordon, Proc. Natl. Acad. Sci. U.S.A. 89, 9176-9180, 1992
A;Title: Characterization of Plasmodium falciparum sporozoite surface protein 2.
A;Reference number: A46283; MuID:93028427; PMID:1409621

A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-574 < ROG A; A; Cross-references: UNIPROT: Q26020; GB: M94013; NID: g160690; PID: g160691 F; 240-287/ Domain: thrombospondin type 1 repeat homology < THR1>

Gaps ö Query Match 100.0%; Score 42; DB 2; Length 574; Best Local Similarity 100.0%; Pred. No. 1.3; Matches 9; Conservative 0; Mismatches 0; Indels

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109 KNKEKALII 117 1 KNKEKALII 9 g õ

Gaps

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A;Residues: 1-468 <AQF>
A;Cross-references: UNIPROT:067281; GB:AE000730; NID:g2983674; PIDN:AAC07253.1; PID:g2983
A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein At2927740 [imported] - Arabidopsis thaliana hypothetical protein At2927740 [imported] - Arabidopsis thaliana (mouse-ear cress) [c]Species: Arabidopsis thaliana (mouse-ear cress) [c]Species: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004 [c]Accession: D84676 [c]Accession: D84676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q9ZUX5; GB:AE002093; NID:g3860258; PIDN:AAC73026.1; GSPDB:GN(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 392, 353-358, 1998
A,Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A,Reference number: A70300; MUID:98196666; PMID:9537320
                                                                                                                                                                    A.Gene: murE; BU221
C.Superfamily: UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diaminopimelate ligase
C.Keywords: ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: F70406
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conserved hypothetical protein ad_1236 - Aquifex aeolicus
C,Species: Aquifex aeolicus
C,Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C,Accession: F70406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 2; Length 468;
Pred. No. 18;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                         2; Length 497
                                                                                                                                                                                                                                                                                                                                         88.1%; Score 37; DB
88.9%; Pred. No. 12;
tive 0; Mismatches
                                A,Cross-references: GB:AP000398; GSPDB:GN00144
A,Experimental source: strain APS
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 88.9
Matches 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      435 KNKEKILII 443
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A,Molecule type: DNA
A,Residues: 1-174 <STO>
A; Residues: 1-497 <STO>
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F70406
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A84956
DD-N-acetylmuramoylalanyl-D-glutamate-2,6-diamino-pimelate ligase (EC 6.3.2.13) [import C;Species: Buchnera sp.
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 03-Jun-2002
C;Accession: A84956
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A;Accession: A84930; MUD:20445173; PMID:10993077
A;Accession: A84956
A;Accession: A84956
A;Accession: A84956
A;Accession: A84956
A;Accession: A84966
                                                                                                                           modulates DNA topology [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD1251
R;Glager, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Jonnaguez-Berranial, G.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jonnes, L.M.; Karet, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma Aptuhors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Reference number: AB1077; MUD:21537279; PMID:11679669
A;Accession: AD1251
A;Status: preliminary
A;Molecule type: DNA
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A;Molecule type: DNA
A;Residues: 1-177 <SAN>
A;Cesidues: 1-177 <SAN>
C;Genetics: Chipper Color (Color of the Color of the Colo
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C;Genetics:
A;Gene: lmo1412
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C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: 570846
C;Accession: 570846
R;Sanchez-Campillo, M.; Dramsi, S.; Gomez-Gomez, J.M.; Michel, E.; Dehoux, P.; Cossart, Mol. Microbiol. 18, 801-811, 1995
A;Title: Modulation of DNA topology by flaR, a new gene, from Listeria monocytogenes.
A;Reference number: S70846; MUID:96422467; PMID:8825084
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Matches 8; Conservative
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Matches 8; Conservative
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C,Accession: A8321
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bri
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoc
A;Reference number: A82950; MUID:20437337; PMID:10984043
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Watare 407, 81-86, 2000
Filtle: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. Al
Reference number: A84930; MUID:20445173; PMID:10993077
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A;Experimental source: strain PAO1
Cross-references: UNIPROT:Q06062; EMBL:L13026; NID:g294339; PIDN:AAD15231.1; PID:g29434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alginate o-acetyltransferase AlgF PA3550 [imported] - Pseudomonas aeruginosa (strain PAO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Buchnera sp.
Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Species: Pseudomonas aeruginosa
;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
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Pred. No. 21;
2; Mismatches 0; Indels
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Pred. No. 34;
1; Mismatches 0; Indels
                                                                                                                                       A,Gene: algF
C,Superfamily: Pseudomonas aeruginosa algF protein
P;1-28/Domain: signal sequence #status predicted <SIG>
F;29-216/Product: algF protein #status experimental <MAT>
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Superfamily: Pseudomonas aeruginosa algF protein
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity 87.5%;
Matches 7; Conservative
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Best Local Similarity 75.0°
Matches 6; Conservative
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                                                         A;Molecule type: protein A;Residues: 29-39 <SHI2>, C;Genetics:
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A;Residues: 1-350 <STO>
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                               A; Accession: S38858
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                                                                             RESULT 8
(297345
PP-loop superfamily ATPase, confers aluminum resistance [imported] - Clostridium acetobu
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: C97345
R;Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q; Gibson, R.; Lee,
J; Daly, M.J; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
J; Bacteriol. 183, 4823-4838, 2001
A;Reference number: A96900; MUD:21359325; PMID:21359325
A;Accession: C97345
A;Accession: C97345
A;Accession: C97345
A;Accession: C97345
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A;Cross-references: UNIPROT:Q97D53; GB:AE001437; PIDN:AAK81550.1; PID:g15026727; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
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Mol. Microbiol. 9, 1027-1035, 1993
A;Title: Nucleotide sequence and expression of the Pseudomonas aeruginosa algF gene cont
A;Reference number: S37351; MUID:95020624; PMID:7934909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA'
A;Residues: 1-4919 <WAR>
A;Cresidues: 1-4919 <WAR>
C;Genetics: C;Genetics: UNIPROT:Q9ZHLO; EMBL:AF057696; NID:G3929021; PID:G3929023; PIDN:AAC7
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C;Species: Haemophilus ducreyi
C;Species: Haemophilus ducreyi
C;Species: Haemophilus ducreyi
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31105
R;Ward, C.K.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J.
J. Bacteriol. 180, 6013-6022, 1998
A;Title: Haemophilus ducreyi secretes a filamentous hemagglutinin-like protein.
A;Reference number: 220984; MUID:99030326; PMID:9811662
A;Accession: T31105
A;Accession: T31105
A;Stausus: preliminary; translated from GB/EMBL/DDBJ
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C;Species: Pseudomonas aeruginosa
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: S37351; S388878888;Shinabarger, D::Mav P B : B.
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87.5%; Pred. No. 2.8e+02;
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A;Gene: CAC3627
C;Superfamily: conserved hypothetical protein HI1191
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Pred. No. 14;
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les 7; Conservative
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A,Molecule type: DNA
A,Residues: 1-216 <SHI1>
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Search completed: December Job time: 24.5 secs
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284 QNKEKALAI 292
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F96570

UNKnown protein, 80333-82175 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: F96570
C;Accession: F96570
C;Accession: F96570
C;Accession: F96570
C;Accession: F96570
A;Authors: Hughes, B; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: F96570
A;Status: preliminary
A;Residues: 1-320 <ATO.
A;Cross-references: UNIPROT:Q9C928; GB:AE005173; NID:g6862953; PIDN:AAF30341.1; GSPDB:GN
C;Generics: F14674 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gross-references: UNIPROT:Q66619; GB:U20824; NID:g695172; PIDN:AAC13823.1; PID:g695208
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995
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                                                                                                                                                                          hypothetical protein 35 - equine herpesvirus 2

C;Species: equine herpesvirus 2

C;Date: 27-0ct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C;Accession: S55530

R;Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.

J. Mol. Biol. 249, 520-528, 1995

A;Title: The DNA sequence of equine herpesvirus 2.

A;Reference number: S55594; MuID:95302501; PMID:7783207

A;Accession: S5530

A;Accession: S5530

A;Reference preliminary; nucleic acid sequence not shown; translation not shown

A;Residues: 1-154 <TEL>
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N;Alternate names: peptide chain release factor 2
C;Species: Synechocystis sp.
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A;Map position: 1
C;Superfamily: probable membrane protein YOLO77c
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Best Local Similarity 75.0
Thea 6; Conservative
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Cidate: 25-Apr-1997 #Sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
Cidate: 25-Apr-1997 *C. course
Cidate: 25-Apr-1997 #Sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
Cidate: 25-Apr-1997 *St448
Airansko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
DNA Res. 3, 109-136, 1996
Airitle: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
Airitle: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
Airitle: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
Airitle: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
Airitle: Sequence analysis of the genome of the Embination of Shates: nucleic acid sequence not shown; translation not shown
Airitle: Sequence analysis of the genome of the Embination of Embination of Empire and UAA.
Airitle: Sequence of two codon-specific peptide-chain-release factors that are respond codons UGA and UAA.
Cicomment: The gene coding for this protein (RP-2) contains a UGA in-frame termination of codons UGA and UAA.
Cicomment: The gene coding for this protein to regulate its own production.
Cicomment: The gene coding factor
Cicoment: The gene c
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plasmodium

09tyc6 plasmodium 09tyc8 plasmodium 09tyc8 plasmodium 09tyd0 plasmodium 09tyd1 plasmodium 09tyd2 plasmodium 09tyd2 plasmodium Aaq11891 plasmodiuu Aaq11892 plasmodiu Aaq11894 plasmodiu Aaq11895 plasmodiu Aaq11895 plasmodiu

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Trap protein (Fragment).
Name-trap;
Name-trap;
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mamillapalli A., Joshi H., Malhotra P.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ58171; CAE46498.1;
InterPro; IPR000884; TSP1.
InterPro; IPR002035; WWF A.
Pfam; PF00090; TSP 1; 1.
Pfam; PF00090; TSP 1; 1.
Pfam; PR00092; WWA_1.
PRINTS; PR00453; WWADOMAIN.
SWART; SMO0327; WWA, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               327 AA; 37251 MW; 881D7A4B4EDD235A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-WAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
Trap protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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SEQUENCE FROM N.A.
STRAIN=DK3-16;
Mamillapalli A., Joshi H., Malhotra P.;
                                                                                                                              AAQ11893
AAQ11894
AAQ11894
AAQ11895
                                                                                                                                                                                                                                                                                                                                        Created)
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09TYCS
09TYC6
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
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PROSITE; PS50234; VWFA; 1.
NON TER 327 327
SEQUENCE 327 AA; 37251 N
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   105 KNKEKALII 113
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CAE46498
CAE46498;
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070gi8 plasmodium
070gk2 plasmodium
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070gk3 plasmodium
076109 plasmodium
076111 plasmodium
076112 plasmodium
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076114 plasmodium
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071508 plasmodium
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                                                                                               December 6, 2004, 15:17:52; Search time 125.5 Seconds (without alignments) 41.262 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                            1825181
                              Compugen Ltd.
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compug
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                                                                                                                                                                                                                                                                 1825181 segs, 575374646 residues
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070GE3
070GE3
070GC3
070GK3
070GK3
CAE46493
CAE46493
CAE46497
TRAP PLAFA
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Maximum Match 100%
Listing first 45 summaries
                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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Match Length DB
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Result g ö

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Length 327; IndelB ô

Gaps

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100.0%; Score 42; DB 2; Length 331; 100.0%; Pred. No. 5; tive 0; Mismatches 0; Indels

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331 AA; 37521 MW; CBD1823A0C8C49EB CRC64;
                                                                                          PRINTS; PRO0453; VWFADDMAIN.
SWART; SM00209; TSP1; 1.
SWART; SM00227; VWA; 1.
PROSITE; PS50234; VWFA; 1.
NON TER 331 331
SEQUENCE 331 AA; 37521 MW;
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Matches 9; Conservative
         Pfam; PF00090; TSP_1; 1.
Pfam; PF00092; VWA; 1.
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"Polymorphism in TRAP N-terminal region of Plasmodium falciparum in Indian isolates.";
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
BMBL, AJS1771; CAE46498.1; -.
NON_TER 327 327
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YCBI_TaxID=5833;
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NCBI_TaxID=5833;
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A Mamillapalli A., Joshi H., Malhotra P.;
C Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ582081; CAE46656.1; -.
R InterPro; IPR000884; TSP1.
R Pfam; PF00090; TSP-1; 1.
R Pfam; PF00090; TSP-1; 1.
R Pfam; PR00453; VWFADOMAIN.
R SMART; SM00209; TSP1; 1.
R SMART; SM00209; TSP1; 1.
R PROSITE; PS50092; TSP1; 1.
R PROSITE; PS50234; VWA; 1.
R PROSITE; PS50234; VWA; 1.
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Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJS81770; CAE46497.1; -.
INTERPRO; IPRO00884; TSP1.
INTERPRO; IPRO02035; VWP.A.
                                                                                                                                                                                                                                                   327 AA; 37251 MW; 881D7A4B4EDD235A CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Trap protein (Fragment).
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Best Local Similarity 100.
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SEQUENCE
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Q70GJ8;
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Q70GB3

ID Q70GB3

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DT 05-J
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Q70GJ8
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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blasmodini Alveolata; Apicomplexa; Haemosporida; Plasmodium.
VGBI_TaxID=5833;
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; Pred. No. 5;
0; Mismatches 0; Indels
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SEQUENCE FROM N.A.

SUBMILLADALLI A., Joshi H., Malhotra P.;

Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ581765; CAE46493.1; -.

InterPro; IPR002084; TSP1.

InterPro; IPR002035; VWF_A.

Pfam; PF00090; TSP_1; 1.

Pfam; PF00092; VWA; 1.
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Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                       331 AA
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SMART; SM00329; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
NON TER 331
SEQUENCE 331 AA; 37609 MW;
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Best Local Similarity 100.0%;
Matches 9; Conservative 0
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109 KNKEKALII 117
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SEQUENCE FROM N.A.
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Gaps

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STRAIN=PP3-12;
Mamillapalli A., Joshi H., Malhotra P.;
Mamillapalli A., Joshi H., Malhotra P.;
"Polymorphism in TRAP N-terminal region of Plasmodium falciparum in Indian isolates.";
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ582081; CAE46626.1; -... nipproparts AJ582081; AJ582081; CAE46626.1; -... nipproparts AJ582081; AJ5
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STRAIN=CM3-56;
Mamillapalli A., Joshi H., Malhotra P.;
"Polymorphism in TRAP-N terminal region of Plasmodium falciparum in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5833;
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                                                                                                                                                                          Length 331;
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Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJS81770; CAS6497.1; -.
NON TER 331 331 331
                                                                                   SEQUENCE 331 AA; 37609 MW; 2FE4EB47F1963D76 CRC64;
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SEQUENCE 331 AA; 37521 MW; CBD1823A0C8C49EB CRC64;
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
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02-WAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
Trombospondin-related protein (Fragment).
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EMBL; AJ581765; CAE46493.1; -.
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Matches 9; Conservative
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CAE46626
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STRAIN=RM3-21;
Mamillapalli A., Joshi H., Malhotra P.;
Mamillapalli A., Joshi H. Karminal region of Plasmodium falciparum in Indian isolates.";
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
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Mamillapalli A., Joshi H., Malhotra P.;
"Polymorphism in TRAP-N terminal region of Plasmodium falciparum in
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum.
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI TaxID=5833;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 42; DB 2; Length 331; 100.0%; Pred. No. 5; ive 0; Mismatches 0; Indels
                                INTERPRO 1 PRO00884; TSP1.
INTERPRO; IPRO00884; TSP1.
INTERPRO 1 PRO00015; VWF_A.
Pfam; PF00002; VWA; 1.
PRINTS; PR00453; VWFABDOMAIN.
SWART; SM00209; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
PROSITE; PS50234; VWFA; 1.
PNOSITE; PS50234; VWFA; 1.
NON TER 331 AA; 37625 MW; 4258443729D48835 CRC64;
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Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ581764; CAE46492.1; -.
NON TER 331 331.
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331 AA; 37625 MW; 4258443729D48835 CRC64;
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Trap protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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    EMBL; AJ581764; CAE46492.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity luv...
9; Conservative
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CAE46492;
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CAE46493;
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CAE46492
ID CAE4
AC CAE4
DT 02-M
DT 02-M
DT 02-M
DT 02-M
DT TAPP
CO NTAPP
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CAE46433
CAE46433
DC CAE4
AC CAE4
DT 02-M
DT 
S T T D R R D R R D R R D R R D R R D R R D R R D R R D R R D R R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R D R 
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Jongwattiwes S., Putaporntip C., Kanbara H., Tanabe K.;
Jongwattiwes S., Putaporntip C., Kanbara H., Tanabe K.;
"Variation in the thrombospondin-related adhesive protein (TRAP) gene
of Plasmodium Falciparum from Thai field isolates.";
Mol. Biochem. Parasitol. 92:349-353 (1998).
EMBL, AB006331; BAA31167.1; -.
InterPro; IPR000894; TSP1.
InterPro; IPR000995; VWP_A.
Pfam; PP00092; VWA, 1.
SMART; SM00209; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
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MEDLINE=98119420; PubMed=9657338;
MEDLINE=98119420; PubMed=9657338;
MODULINE=98119420; PubMed=9657338;
MODULINE=98119420; PubMed=9657338;
MODULINE=1000000; Pubmontopondin-related adhesive protein (TRAP) gene of Plasmodium falciparum from Thai field isolates.";
MOLI Biochem. Parasitol. 92:349-353(1998).
INTERPO: IPRO00884; TSP1.
InterPro; IPRO00884; TSP1.
InterPro; IPRO00095; WP-A.
Pfam; PF00090; TSP 1; 1.
Pfam; PF00090; TSP 1; 1.
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NCBL_TaxID=5833;
                                                                                                                                                                                                                                                                           Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 42; DB 2; Length 559; 100.0%; Pred. No. 8.4;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                   559 AA
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                                                                                                                                                                                                                                    Thrombospondin-related protein (Fragment).
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                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=98319420; Pubmed=9657338;
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SMART; SM00327; VWA; 1.
PROSITE; PS50092; TSP1; 1.
PROSITE; PS50234; VWFA; 1.
NON TER 559 559
SEQÜENCE 559 AA; 63304 MY
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  109 KNKEKALII 117
                                                                                                                                                                                                                                                               Plasmodium falciparum.
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                      NCBI_TaxID=5833;
                                                                                                                                                                                        01-NOV-1998
01-MAR-2002
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SEQUENCE
                                                                                                                                                                                                                                                                                     Eukaryota;
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076111
                                                                    RESULT 12
076109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Potential.
Thrombospondin related anonymous protein
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                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=88318952; PubMed=3045563; Robson K.J.H., Hall J.R.S., Jennings M.W., Harris T.J.R., Marsh K., Newbold C.I., Tate V.E., Weatherall D.J.; Halphy conserved amino-acid sequence in thrombospondin, properdin and in proteins from sporozoites and blood stages of a human malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 335:79-82(1988).
-!- DEVELOPMENTAL STAGE: Expressed during erythrocytic stage of life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antigen; Cell adhesion; Glycoprotein; Malaria; Signal; Transmembrane SIGNAL 1 25
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TSP type-1.
Teogluctamyl lysine isopeptide (Gln-Lys) (interchain with K-? in Factor 3(A)) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isoglutamyl lysine isopeptide (Gln-Lys) (interchain with K-? in Factor 3(A))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-linked (GlcNAc. .) (Potential)
N-linked (GlcNAc. .) (Potential)
N-linked (GlcNAc. .) (Potential)
N-linked (GlcNAc. .) (Potential)
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                                                                                                                                                                                                                                                                                       Plasmodium falciparum.
Bukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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                                                                                                                                                                                        01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-0CT-2004 (Rel. 45, Last annotation update)
Thrombospondin related anonymous protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Contains 1 TSP type-1 domain.
                                                                                                                                           559 AA
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Interpro; IPR000884; TSP1.
Interpro; IPR002035; VWF.A.
Pfam; PF00099; TSP 1; 1.
Pfam; PF00092; VWA; 1.
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SMART; SM00209; TSP1; 1.
SMART; SM00327; VWA; 1.
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PROSITE; PS50234; VWFA; 1.
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310
460
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109 KNKEKALII 117
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310
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559 AA;
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                                                                                                                     TRAP_PLAFA
ID TRAP_PLAFA
AC P16893;
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PROSITE; PS50234; VWFA; 1.
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"Variation in the thrombospondin-related adhesive protein (TRAP) gene of Plasmodium falciparum from Thai field isolates.";
Mol. Biochem. Parasitol. 92:349-353(1998).
InterPro; IPR000884; TSP1.
InterPro; IPR002035; WWF.A.
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"Variation in the thrombospondin-related adhesive protein (TRAP) gene
of Plasmodium falciparum from Thai field isolates.";
Mol. Biochem. Parasitol. 92:349-353(1998).
EMBL, AB006336, BAA31172.1;
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01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Thrombospondin-related protein (Fragment).
Plasmodium falciparum.
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TAXID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TAXID=5833;
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                                               0; Indels
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100.0%; Pred. No. o. o. o. o. Mismatches
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Pred. No. 8.4;
       Pred. No. 8.4;
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                                           Mismatches
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01-NOV-1998 (TrEMBLrel. 08, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
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SEQUENCE FROM N.A.
MEDLINE=98319420; PubMed=9657338;
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MEDLINE=98319420; PubMed=9657338;
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Best Local Similarity 100.0%;
Matches 9; Conservative 0
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Pfam; PF00002; VWN; 1.
SMART; SM00209; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
PROSITE; PS50234; VWRA; 1.
PROSITE; PS50234; VWRA; 1.
PROSITE; PS50234; VWRA; 1.
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Best Local Similarity
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O76112
AC O76112;
DT 01-NOV-1)
DT 01-NOV-1
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O76113
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Sequence 19, Appl
                                                                             December 6, 2004, 15:26:21; Search time 99 Seconds (without alignments) 32.420 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-110-653-624-8
US-110-833-745-8
US-110-833-744-8
US-110-079-167-41
US-110-079-167-41
US-110-653-624-41
US-110-633-439-41
US-110-833-744-41
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                                                                                                                                                                                                                                                 1582122 segs, 356623098 residues
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                                                                                                                                                                                                                                                                                                                                                    Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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ALIGNMENTS

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Sequence 17, Application US/10042202
Publication No. US2020136733A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
CAtherine Elizabeth Margaret ALLSOPP, Ajit LALVANI, Magdalena
PLEBANSKT, Hilton Carter WHITTLE,
ITILE OF INFORMATION: MALARIA PEPTIDES
NUMBER OF SEQUENCES. 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: WENDERCOTH, LIND & PONACK, L.L.P.
STREET: 20.3 K Street, N.W., Suite 800,
CITY: Washington
STATE: D.C.,
COUNTRY: U.S.A.
ZIP: 20006-1021
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDEAG OF WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/10/42,202
FILING DATE: 28-JAN-1997
APPLICATION NUMBER: GB 9406492.0
FILING DATE: 28-JAN-1995
APPLICATION NUMBER: GB 9406492.0
FILING DATE: 30-MAR-1095
APPLICATION NUMBER: GB 9406492.0
FILING DATE: 31-MAR-1095
APPLICATION NUMBER: 23-JAN-1995
APPLICATI
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APPLICANT: Hill, Asian V.S.
APPLICANT: Gilbert, Sarah C.
APPLICANT: Schneider, Jorg
APPLICANT: Schneider, Jorg
APPLICANT: Hanke, Tomas
APPLICANT: Hanke, Tomas
APPLICANT: Smith, Geoffrey L.
APPLICANT: Smith, Geoffrey L.
APPLICANT: Smith, Geoffrey L.
APPLICANT: Shith, Geoffrey C.
APPLICANT: Shith, Geoffrey 
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Pred. No. 0.27;
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; OTHER INFORMATION: CTL Epitope of the Malaria String
US-10-079-167-8
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                            PRIOR FILING DATE: 1997-06-09
PRIOR APPLICATION NUMBER: PCT/GB01/04116
PRIOR PILING DATE: 2001-09-13
PRIOR PILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 11
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PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: PCT/GB98/01681
PRIOR FILING DATE: 1998-06-09
PRIOR FILING DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 11
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Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Unknown
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Sequence 19, Application US/10360836

Sublication No. US20030185854A1

GENERAL INFORMATION:

APPLICANT: Eavial Fidel

APPLICANT: Birkett, Ashley

TITLE OF INVENTION: ADM MALIGNANCIES

FILE REFERENCE: 5986/10376

CURRENT APPLICATION NUMBER: US/10/360,836

CURRENT FILING DATE: 2003-02-07

PRIOR PULING DATE: 2002-02-08

NUMBER OF SEQ ID NOS: 86

SOFTWARE FRANCE: FRANCES OF WINDOWS VERSION 3.0

SOFTWARE FRANCES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 42; DB 13; 100.0%; Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 42; DB 14; 100.0%; Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Publication No. US20030138454A1
GENERAL INFORMATION:
APPLICANT: Hill, Adrian V.S.
APPLICANT: McShane, Helen
APPLICANT: Gilbert, Sarah C.
APPLICANT: Senece, William
APPLICANT: Schneider, Joerg
TITLE OF INVENTION: Vaccination Method
FILE REFERENCE: 2907.1000-001
CURRENT APPLICATION NUMBER: US/10/079,167
CURRENT FILING DATE: 2002-02-19
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1998-06-09
                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-042-202-17
TELECOMMUNICATION INFORMATION
                                                                   (202) -721-8250
                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                               INFORMATION FOR SEQ 1D NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                   TELEPHONE: (202)-721
                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Conservative
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Best Local Similarity
Matches 9; Conserva
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; ORGANISM: Plasmodium
US-10-360-836-19
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Best Local Similarity
                                                                      TELEFAX:
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LENGTH: 9
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hill, Adrian V.S.
APPLICANT: Hill, Adrian V.S.
APPLICANT: Glibert. Sarah C.
APPLICANT: Schneider. Joach C.
APPLICANT: Schneider. Joach C.
APPLICANT: Schneider. Joach C.
APPLICANT: Blanchard, Tomas
APPLICANT: Blanchard, Tom
TITLE OF INVENTION: Mhchods and Reagents for Vaccination
TITLE OF INVENTION: Mhchods and Reagents For Vaccination
TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response
FILE REFERENCE: 2907.100.000
CURRENT APPLICATION NUMBER: US/10/686,943
FRIOR APPLICATION NUMBER: US/09/454,204
PRIOR FILING DATE: 1999.10-16
PRIOR FILING DATE: 1998-10-06
PRIOR FILING DATE: 1998-06-09
PRIOR PILING DATE: 1998-06-09
PRIOR PILING DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                              Length 11;
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100.0%; Pred. No. 0.27;
tive 0; Mismatches 0; Indels
                                                                         Query Match 100.0%; Score 42; DB 17; Length 1 Best Local Similarity 100.0%; Pred. No. 0.27; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; OTHER INFORMATION: CTL Epitope of the Malaria String
US-10-833-744-8
; OTHER INFORMATION: CTL Epitope of the Malaria String
US-10-833-745-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/10686943
Publication No. US20040213799A1
                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/10833744 Publication No. US20040197349A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: McMichael, Andrew
APPLICANT: Hill, Adrian V.S.
APPLICANT: Gilbert, Sarah C.
APPLICANT: Schneider, Jorg
APPLICANT: Plebanski, Magdalena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
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APPLICANT: Hill, Adrian V.S.
APPLICANT: Hill, Adrian V.S.
APPLICANT: Gilbert, Sarah C.
APPLICANT: Gilbert, Sarah C.
APPLICANT: Schneider, Jorg
APPLICANT: Schneider, Jorg
APPLICANT: Plebanski, Magdalena
APPLICANT: Blanchard, Tom
APPLICANT: Blanchard, Tom
TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response
FILE REFERENCE: 2097.1000.000
CURRENT FILING DATE: 2004-04-28
FRIOR APPLICATION NUMBER: US/10/686,943
PRIOR PLILING DATE: 2003-10-16
PRIOR PLILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-10-06
PRIOR FILING DATE: 1999-06-09
PRIOR FILING DATE: 1999-06-09
PRIOR FILING DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 78
NUMBER OF SEQ ID NOS: 78
SOFTMARE: FastSEQ for Windows Version 4.0
                                                                                                                       APPLICANT: Hanke, Tomas APPLICANT: Hanke, Tomas APPLICANT: Hanke, Tomas APPLICANT: Banth, Geoffrey L. APPLICANT: Blanchard, Tom TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response FILE REFERENCE: 2907.1000-000.

CURRENT APPLICATION NUMBER: US/10/686,943
PRIOR PLILING DATE: 2003-10-16
PRIOR PLILING DATE: 2003-10-16
PRIOR PLILING DATE: 1999-12-09
PRIOR PLILING DATE: 1999-12-09
PRIOR PLILING DATE: 1998-06-09
PRIOR PLILING DATE: 1998-06-09
PRIOR FILING DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 78
SOOTHWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: CTL Epitope of the Malaria String
US-10-833-439-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-833-745-8
; Sequence 8, Application US/10833745
; Publication No. US20040191272A1
; GENERAL INFORMATION:
                                                                            Schneider, Jorg
Plebanski, Magdalena
                           Hill, Adrian V.S.
Gilbert, Sarah C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KNKEKALII 9
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ORGANISM: Unknown
FEATURE:
                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Hill, Adrian V.S.
APPLICANT: Hill, Adrian V.S.
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Schneider, Jorg
; APPLICANT: Schneider, Jorg
; APPLICANT: Plebanski, Magdalena
; APPLICANT: Blanchard, Toms
; APPLICANT: Blanchard, Tom
; TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response
; TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response
; TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response
; TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response
; FILE REFERENCE: 2907.100-000
; CURRENT APPLICATION NUMBER: US/10/653,624
; FRIOR APPLICATION NUMBER: US/09/454,204A
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; PRIOR PLILING DATE: 1998-06-09
; PRIOR FILING DATE: 1998-06-09
; RIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 229
                             US20040131594A1
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JS-10-833-439-41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 42; DB 17; Length 11; Best Local Similarity 100.0%; Pred. No. 0.27; Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: CTL Epitope of the Malaria String US-10-686-943-8
CURRENT FILING DATE: 2003-10-16
PRIOR APPLICATION NUMBER: US/09/454,204
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR PILING DATE: 1999-16-09
PRIOR PILING DATE: 1999-06-09
PRIOR PILING DATE: 1990-06-09
PRIOR PILING DATE: 1990-06-09
PRIOR FILING DATE: 1990-06-09
SPIOR FILING DATE: 1990-06-09
SPIOR FILING DATE: 1990-06-09
SOFTWARE: FABLSEQ for Windows Version 4.0
ELENGTH: 11
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APPLICANT: Hill, Adrian V.S.
APPLICANT: McShane, Helen
APPLICANT: Gilbert, Sarah C.
APPLICANT: Reece, William
APPLICANT: Schneider, Joerg
TITLE OF INVENTION: Vaccination Method
FILE REFERENCE: 2907.1000-001
CURRENT FILING DATE: 2007.02-19
PRIOR APPLICATION NUMBER: US/10/079,167
CURRENT APPLICATION NUMBER: US/10/079,167
CURRENT FILING DATE: 1999-12-09
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: CRT/GB98/01681
PRIOR APPLICATION NUMBER: BT/GB98/01681
PRIOR FILING DATE: 1997-06-09
PRIOR FILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: PCT/GB01/04116
PRIOR FILING DATE: 2001-09-13
PRIOR PILING DATE: 2001-09-13
PRIOR PRILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FEASTSQ FOR WINDOWS VERSION 4.0
SEQ ID NO 41
LENGTH: 229
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Sequence 41, Application US/10079167

Publication No. US20030138454A1

GREBAL INFORMATION:
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Unknown
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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APPLICANT: Gilbert, Sarah C.
APPLICANT: Gibert, Sarah C.
APPLICANT: Schneider, Jorg
APPLICANT: Plebanski, Magdalena
APPLICANT: Hanke, Tomas
APPLICANT: Blanchard, Tom
TITLE OF INVENTION: Methods and Reagents for Vaccination
TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response
                                                                                                100.0%; Score 42; DB 16; Length 229; 100.0%; Pred. No. 6;
                                                                                                                                                 Indels
; FEATURE:
; OTHER INFORMATION: Complete Epitope of Malaria String
US-10-653-624-41
                                                                                                                                                 o'
                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TILLE REFERENCE: 2907.1000-000
CURRENT APPLICATION NUMBER: US/10/833,439
CURRENT FILING DATE: 2004-04-28
PRIOR APPLICATION NUMBER: US/10/686,943
PRIOR PILING DATE: 2003-10-16
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1998-06-09
SPRIOR FILING DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PRESEE OF WINDOWS VETSION 4.0
SEQ ID NO 41
LENGTH. 229
                                                                                                                                                                                                                                                                                                                                                                      Sequence 41, Application US/10833439
Publication No. US20040175365A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: McMichael, Andrew
                                                                                             Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                       58 KNKEKALII 66
                                                                                                                                                                                                   1 KNKEKALII 9
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ORGANISM: Unknown
FEATURE:
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RESULT 10 US-10-653-624-41 ; Sequence 41, Application US/10653624

58 KNKEKALII 66

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SEGEMENT INFORMATION:

APPLICANT: MCMIChael, Andrew
APPLICANT: Hill, Adrian V.S.
APPLICANT: Hill, Adrian V.S.
APPLICANT: Hill, Adrian V.S.
APPLICANT: Schneider, Jorg
APPLICANT: Blancher, Jorg
APPLICANT: Blancherd, Tomas
APPLICANT: Blancherd, Tomas
APPLICANT: Blancherd, Tom
TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response
TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response
FILE REFERENCE: 2907.1000-000
CURRENT APPLICATION NUMBER: US/10/686,943
CURRENT FILING DATE: 1999-12-09
FRIOR FILING DATE: 1999-12-09
FRIOR FILING DATE: 1999-12-09
FRIOR FILING DATE: 1997-06-09
NUMBER: OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41
LENGTH: 229
FURNER FOR A PROBLEM TO THE STATE TO THE STA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Complete Epitope of Malaria String US-10-833-744-41
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                                               PRIOR APPLICATION NUMBER: US/10/686,943
PRIOR FILING DATE: 2003-10-16
PRIOR PILING DATE: 2003-10-16
PRIOR PILING DATE: 1999-12-09
PRIOR FILING DATE: 1998-06-09
PRIOR PLING DATE: 1998-06-09
PRIOR PILING DATE: 1998-06-09
PRIOR PILING DATE: 1998-06-09
PRIOR PRIOR DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 78
SEOTHWARE: FASESEQ FOR WINDOWS VERSION 4.0
SEOTHWARE: PASESEQ FOR WINDOWS VERSION 4.0
SEOTHWARE: PASESEQ FOR WINDOWS VERSION 4.0
SEOTHWARE: PASESEQ FOR WINDOWS VERSION 4.0
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Publication No. US20040213799A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Unknown
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                                                                                                                                                                                Gaps
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APPLICANT: Plebanski, Magdalena
APPLICANT: Hanke, Tomas
APPLICANT: Hanke, Tomas
APPLICANT: Blanchard, Tomas
APPLICANT: Blanchard, Tom
TITLE OF INVENTION: Methods and Reagents for Vaccination
TITLE OF INVENTION: Mhich Generate A CD8 T Cell Immune Response
FILE REFERENCE: 2007.1000-000
CURRENT FILING DATE: 2003-10-16
PRIOR PILING DATE: 2003-10-16
PRIOR FILING DATE: 1999-12-09
PRIOR PILING DATE: 1999-06-09
PRIOR PILING DATE: 1998-06-09
PRIOR FILING DATE: 1999-06-09
PRIOR FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response
FILE REFERENCE: 2907.1000-000
                                                                                                      Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 42; DB 17; Length 229; Best Local Similarity 100.0%; Pred. No. 6; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                        0; Indels
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OTHER INFORMATION: Complete Epitope of Malaria String
                                                                                               Query Match 100.0%; Score 42; DB 16; Best Local Similarity 100.0%; Pred. No. 6; Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 41, Application US/10833745
Publication No. US20040191272A1
GENERAL INFORMATION:
APPLICANT: MCMichael, Andrew
APPLICANT: Hill, Adrian V.S.
APPLICANT: Gilbert, Sarah C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 41, Application US/10833744 Publication No. US20040197349A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                      58 KNKEKALII 66
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ORGANISM: Unknown
       ) OIREN 110-833-439-41
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US-10-437-963-105530

Sequence 105530, Application US/10437963

Bedication No. US20040123343A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: A Rosa, Thomas J.
APPLICANT: Tou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Roukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 105530

LENGTH: 119
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92.9%; Score 39; DB 16; Length 119;
Best Local Similarity 77.8%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT:
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_102766C.1.pep
US-10-437-963-105530
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Search completed: December 6, 2004, 15:36:08 Job time : 100 secs

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